

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:54:28 ; Search time 2925.11 Seconds  
(without alignments)  
7749.596 Million cell updates/sec

Title: US-09-733-368A-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgtccctgtgtgtgtt.....accacattgtgtgacatc 523

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	523	100.0	648	6	AX175190	AX175190 Sequence
2	523	100.0	648	6	AX175195	AX175195 Sequence
3	519.8	99.4	7086	6	AX743955	AX743955 Sequence
4	517.8	99.0	2245	6	AX643582	AX643582 Sequence
5	517.8	99.0	6289	12	XXU42373	U42373 Cloning vec
6	515.6	98.6	3256	14	ALRDA2	L29199 Rous sarcom
7	515	98.5	4965	6	AR071323	AR071323 Sequence
8	514	98.3	1016	14	REASV3	V01167 Avian sarco
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ALIGNMENTS

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LOCUS Sequence 1 from Patent WO0142444.  
DEFINITION  
ACCESSION AXI75190  
VERSION AXI75190.1 GI:14598581  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Rivera, V., Zoltick, P. and Wilson, J.M.  
TITLE Methods for expression of genes in primates  
JOURNAL Patent: WO 0142444-A 1 14-JUN-2001;  
ARIAD GENE THERAPEUTICS, INC. (US); THE UNIVERSITY OF PENNSYLVANIA (US)

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Best Local Similarity 100.0%; Pred. No. 3.2e-148;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DEFINITION  
ACCESSION AXI75195  
VERSION AXI75195.1 GI:14598586  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Rivera, V., Zoltick, P. and Wilson, J.M.  
TITLE Methods for expression of genes in primates  
JOURNAL Patent: WO 0142444-A 6 14-JUN-2001;  
ARIAD GENE THERAPEUTICS, INC. (US); THE UNIVERSITY OF PENNSYLVANIA (US)

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Best Local Similarity 100.0%; Pred. No. 3.2e-148;  
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LOCUS AX743955 7086 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 3 from Patent WO03031630.
ACCESSION AX743955
VERSION AX743955.1 GI:30722652
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1.
AUTHORS Pazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
TITLE Multi-clonronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 3 17-APR-2003;
Keryos Spa (IT)
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LOCUS AX643582 2245 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 1 from Patent WO02099100.
ACCESSION AX643582
VERSION AX643582.1 GI:28551382
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE
1.
AUTHORS Al-Rubeai, M. and Shuttleworth, J.
TITLE Method of production of a protein in cells which inducibly express the cell cycle inhibitor protein, p21
JOURNAL Patent: WO 02099100-A 1 12-DEC-2002;
Lonza Biologics plc (GB)
FEATURES
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LOCUS XXU42373 6289 bp DNA circular SYN 05-JAN-1996
DEFINITION Cloning vector pOP13Cat target vector from Lacswitch System.
ACCESSION U42373
VERSION U42373.1 GI:1147762
KEYWORDS Cloning vector pOP13Cat
SOURCE Cloning vector pOP13Cat
ORGANISM Cloning vector pOP13Cat
REFERENCE 1 (bases 1 to 6289)
AUTHORS Marsh, S.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1995) Sam Marsh, Marketing, Stratagene, 11011
North Torrey Pines Road, La Jolla, CA 92037, USA
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Best Local Similarity 99.6%; Pred. No. 1.3e-146;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 6

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ALRDA2
LOCUS Rous sarcoma virus 3256 bp DNA linear VRL 12-APR-1999
DEFINITION Rous sarcoma virus (Schmidt-Ruppin A) env-src-3'LTR.
ACCESSION L29199 J02018 J02026 J02352 K01194 K01195 N00021
VERSION L29199.1 GI:459672
KEYWORDS c-myc proto-oncogene; kinase; protein kinase; src oncogene.
SEGMENT 2 of 2
SOURCE Rous sarcoma virus
ORGANISM Rous sarcoma virus
REFERENCE 1 (sites)
AUTHORS Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
TITLE Czerlilofsky, A.P., DeLorbe, W., Swanstrom, R., Varmus, H.E., Bishop, J.M.,
Bishop, J.M., Fischer, E. and Goodman, H.M.
The nucleotide sequence of an untranslated but conserved domain at
the 3' end of the avian sarcoma virus genome
Nucleic Acids Res. 8 (13), 2967-2984 (1980)
JOURNAL 81053726
MEDLINE 6253899
PUBMED 6253899
REFERENCE 2 (sites)
AUTHORS Czerlilofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M.,
Fischer, E. and Goodman, H.M.
Nucleotide sequence of an avian sarcoma virus oncogene (src) and
proposed amino acid sequence for gene product
Nature 287 (5779), 198-203 (1980)
JOURNAL 81052295
MEDLINE 6253794
PUBMED 6253794
REFERENCE 3 (sites)
AUTHORS Swanstrom, R., DeLorbe, W.J., Bishop, J.M. and Varmus, H.E.
Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA:
viral DNA contains direct and inverted repeats similar to those in
transposable elements
Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
JOURNAL 81223697
MEDLINE 6264426
PUBMED 6264426
REFERENCE 4 (sites)
AUTHORS Swanstrom, R., Varmus, H.E. and Bishop, J.M.
Nucleotide sequence of the 5' noncoding region and part of the gag
gene of Rous sarcoma virus
J. Virol. 41 (2), 535-541 (1982)
JOURNAL 82192582
MEDLINE 6281465
PUBMED 6281465
REFERENCE 5 (sites)
AUTHORS Hughes, S.H.
Sequence of the long terminal repeat and adjacent segments of the
endogenous avian virus Rous-associated virus 0
J. Virol. 43 (1), 191-200 (1982)
JOURNAL 82269131
MEDLINE 6286997
PUBMED 6286997
REFERENCE 6 (sites)
AUTHORS Misra, T.K., Grandgenett, D.P. and Parsons, J.T.
Avian retrovirus pp32 DNA-binding protein. I. Recognition of
specific sequences on retrovirus DNA terminal repeats
J. Virol. 44 (1), 330-343 (1982)
JOURNAL 83059884
MEDLINE 6292495
PUBMED 6292495
REFERENCE 7 (sites)
AUTHORS Czerlilofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M.,
Fischer, E. and Goodman, H.
Corrections to the nucleotide sequence of the src gene of Rous
sarcoma virus
Nature 301 (5902), 736-738 (1983)
JOURNAL 83141780
MEDLINE 6299633
PUBMED 6299633
REFERENCE 8 (sites)
AUTHORS Sorge, J., Ricci, W. and Hughes, S.H.
cis-Acting RNA packaging locus in the 11S-nucleotide direct repeat
of Rous sarcoma virus
J. Virol. 48 (3), 667-675 (1983)
JOURNAL 84036404
MEDLINE 6313966
PUBMED 6313966
REFERENCE 9 (sites)
AUTHORS Hughes, S. and Kosik, E.
Mutagenesis of the region between env and src of the SR-A strain of

```



Rous sarcoma virus for the purpose of constructing

- helper-independent vectors
- JOURNAL  
MEDLINE  
84251740  
6330399  
PUBMED
- REFERENCE  
10 (sites)  
Petersen,R.B., Hensel,C.H. and Hackett,P.B.  
Identification of a ribosome-binding site for a leader peptide  
encoded by Rous sarcoma virus RNA  
J. Virol. 51 (3), 722-729 (1984)
- JOURNAL  
MEDLINE  
84292449  
6068795  
PUBMED
- REFERENCE  
11 (sites)  
Hughes,S., Mellstrom,K., Kosik,E., Tamanoi,F. and Brugge,J.  
Mutation of a termination codon affects src initiation  
Mol. Cell. Biol. 4 (9), 1738-1746 (1984)
- JOURNAL  
MEDLINE  
85036324  
6092936  
PUBMED
- REFERENCE  
12 (sites)  
Resnick,R., Omer,C.A. and Faras,A.J.  
Involvement of retrovirus reverse transcriptase-associated RNase H  
in the initiation of strong-stop (+) DNA synthesis and the  
generation of the long terminal repeat  
J. Virol. 51 (3), 813-821 (1984)
- JOURNAL  
MEDLINE  
84292461  
6206236  
PUBMED
- REFERENCE  
13 (sites)  
Pellman,D., Garber,E.A., Cross,F.R. and Hanafusa,H.  
Fine structural mapping of a critical NH2-terminal region of p60src  
Proc. Natl. Acad. Sci. U.S.A. 82 (6), 1623-1627 (1985)
- JOURNAL  
MEDLINE  
85166183  
2984663  
PUBMED
- REFERENCE  
14 (sites)  
Maroney,A.C., Oureshi,S.A., Foster,D.A. and Brugge,J.S.  
Cloning and characterization of a thermostable v-src gene for use  
in reversible transformation of mammalian cells  
Oncogene 7 (6), 1207-1214 (1992)
- JOURNAL  
MEDLINE  
92278773  
1375718  
PUBMED
- COMMENT  
The bases as they are found in the references are listed below:  
1-3107 Nature 287, 198-203 (1980)  
2907-3256 Proc. Natl. Acad. Sci. U.S.A. 78, 124-128 (1981)  
2244-3176 Nucleic Acids Res. 8, 2967-2984 (1980)  
700-908 J. Virol. 43, 191-200 (1982)  
2927-3176 J. Virol. 44, 330-343 (1982)  
1-3107 Nature 301, 736-738 (1983)  
706-900 and 2791-2930 J. Virol. 48, 667-675 (1983)  
721-1140 Mol. Cell. Biol. 4, 1738-1746 (1984)  
2912-2938 J. Virol. 51, 813-821 (1984)  
873-882 and 990-1128 Virology 136, 89-99 (1984)  
1121-1173 Proc. Nat. Acad. Sci. U.S.A. 82, 1623-1627 (1985) [1]  
revised by [7].  
[7] revises [1].  
See comment in segment 1.  
The src gene is believed to have been obtained from avian DNA when  
an AUV-like virus recombined with host DNA. Homology to the c-src  
gene of chicken begins at position 1032. A direct repeat of about  
100 bp is present near either end of exon 2 the 21S (src) mRNA.  
These repeats include positions 772-899 and 2703-2799. A  
polyadenylation signal is present at position 3149-3154. [7]  
contains a revision of the sequence in [1]. Individual revisions  
are not noted in sites.  
[9] mutated the 'tga' stop codon at position 1057-1059 to 'cga' and  
found that the mutant strain produced an src protein extended at  
the NH-terminal end.  
[10] created a synthetic Rous sarcoma virus lacking the direct  
repeat 5' of src-p60 and with ClaI sites flanking src-p60 to create  
a vector capable of expressing genes inserted in place of src-p60  
(see RSV vector in synthetic sections).  
[11] used mutants with alterations in the N-terminal region of the  
src-p60 gene to determine the requirements for N-myristylation of  
src-p60. The site of addition of myristic acid is the cytosine  
residue at amino acid position 2 (position 1126-1128 of this

sequence).

FEATURES  
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Location/Qualifiers  
1..3256  
/organism="Rous sarcoma virus"  
/proviral  
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/strain="Schmidt-Ruppin A"  
/db\_xref="taxon:11886"  
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/product="35Ss (gag) AND 35Sb (gag-pol), 28S (env) mRNA"  
misc\_RNA  
<1..3176  
/note="35S virion RNA"  
intron  
<1..1047  
/note="21S (src) intron A"  
CDS  
<1..743  
/note="env-Pr95 polyprotein precursor"  
/number=2  
/codon\_start=3  
/protein\_id="AAA42562.1"  
/db\_xref="GI:459676"  
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LDDVTSIBHVLONRAIDFILLAHGCGEDVAGCCFNLSQSESTOKFKOLMKSHV  
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126..740  
/product="glycoprotein-37"  
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/db\_xref="GI:459677"  
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2927..3256  
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conflict  
2938  
/citation=[12]  
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3156..3176  
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Query Match 98.6%; Score 515.6; DB 14; Length 3256;  
Best Local Similarity 99.2%; Pred. No. 5.9e-146;  
Matches 518; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
Db 2668 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTCGCGAGTAAATTTAAGCTACA 2727  
Qy 61 ACAAGGCAAGGCTTACCGCAATTCATGAGATCTGCTTAGGGTTAGGGCTTTGCG 120  
Db 2728 ACAAGGCAAGGCTTACCGCAATTCATGAGATCTGCTTAGGGTTAGGGCTTTGCG 2787  
Qy 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTCTTAGG 180  
Db 2798 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTCTTAGG 2847  
Qy 181 CGAAAAGCGGGCTTCGGTGTGTACGGGTTAGGATCCCTCAGGATATAGTATTTCGC 240  
Db 2848 CGAAAAGCGGGCTTCGGTGTGTACGGGTTAGGATCCCTCAGGATATAGTATTTCGC 2907  
Qy 241 TTTTGCATAGGAGGGGGGAATAGTCTTATGCACTACTCTTGTAGTCTTGCAACATGG 300



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RESULT 9
AX643583
LOCUS AX643583 562 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 2 from Patent WO0209100.
ACCESSION AX643583
VERSION AX643583.1 GI:28551383
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Al-Rubeai,M. and Shuttleworth,J.
TITLE Method of production of a protein in cells which inducibly express
the cell cycle inhibitor protein, p21
JOURNAL Patent: WO 0209100-A 2 12-DEC-2002;
Lonza Biologics plc (GB)
FEATURES
source
1..562
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
/notice="Rous Sarcoma Virus LTR promoter"
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Query Match 98.2%; Score 513.8; DB 6; Length 562;
Best Local Similarity 99.6%; Pred. No. 2e-145;
Matches 515; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CTGCTCCCTGTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db 46 CTGCTCCCTGTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 105
Qy 61 ACAAGCAAGGCTTGACCGACAAATTCATGAGATCTCTGAGGGGACTAGGGTGTGTTAGG 180
Db 106 ACAAGCAAGGCTTGACCGACAAATTCATGAGATCTCTGAGGGGACTAGGGTGTGTTAGG 165
Qy 121 CTGCTTCGCGATGTACGGGCCAGATATTCGATGAGATCTCTGAGGGGACTAGGGTGTGTTAGG 180
Db 166 CTGCTTCGCGATGTACGGGCCAGATATTCGATGAGATCTCTGAGGGGACTAGGGTGTGTTAGG 225
Qy 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGAGTCCCTCAGGATATAGTATTGGC 240
Db 226 CGAAAGCGGGCTTCGGTTGTACGGGTAGAGTCCCTCAGGATATAGTATTGGC 285
Qy 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300
Db 286 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 345
Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
Db 346 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 405
Qy 361 TGGAGTAAAGTGTAGCATCTGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420
Db 406 TGGAGTAAAGTGTAGCATCTGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 465
Qy 421 TTGGCAACCACTAAATTCGGATTGCGAGATATTGATTAAAGTCCCTAGCTCGATA 480
Db 466 TTGGCAACCACTAAATTCGGATTGCGAGATATTGATTAAAGTCCCTAGCTCGATA 525
Qy 481 CAATAAGCCGATTTGACCAATTCACCAATTTGGTGG 517
Db 526 CAATAAGCCGATTTGACCAATTCACCAATTTGGTGG 562
RESULT 10
AX743954
LOCUS AX743954 4457 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 2 from Patent WO03031630.
ACCESSION AX743954
VERSION AX743954.1 GI:30722651

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KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 2 17-APR-2003;
Keryos Spa (IT)
FEATURES
Location/Qualifiers
source
1..4457
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 97.3%; Score 508.8; DB 6; Length 4457;
Best Local Similarity 99.4%; Pred. No. 7e-144;
Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1 CTGCTCCCTGTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db 457 CTGCTCCCTGTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 516
Qy 61 ACAAGCAAGGCTTGACCGCAAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTCGG 120
Db 517 ACAAGCAAGGCTTGACCGCAAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTCGG 576
Qy 121 CTGCTTCGCGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db 577 CTGCTTCGCGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 636
Qy 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGAGTCCCTCAGGATATAGTATTGGC 240
Db 637 CGAAAGCGGGCTTCGGTTGTACGGGTAGAGTCCCTCAGGATATAGTATTGGC 696
Qy 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300
Db 697 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 756
Qy 301 TAAAGTATGATTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
Db 757 TAAAGTATGATTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 816
Qy 361 TGGAGTAAAGTGTAGCATCTGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420
Db 817 TGGAGTAAAGTGTAGCATCTGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 876
Qy 421 TTGAGCAACCACTAAATTCGGATTGCGAGATATTGTRTTTAAAGTCCCTAGCTCGAT 479
Db 877 TTGAGCAACCACTAAATTCGGATTGCGAGATATTGTRTTTAAAGTCCCTAGCTCGAT 936
Qy 480 ACAATAAGCCGATTTGACCAATTCACCAATTTGGTGGCACCTC 523
Db 937 ACAATAAGCCGATTTGACCAATTCACCAATTTGGTGGCACCTC 980
RESULT 11
AX743956/c
LOCUS AX743956 7334 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 4 from Patent WO03031630.
ACCESSION AX743956
VERSION AX743956.1 GI:30722653
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 4 17-APR-2003;
Keryos Spa (IT)
FEATURES
Location/Qualifiers

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/mol_type="genomic DNA"
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ORIGIN
Query Match 97.3%; Score 508.8; DB 6; Length 7334;
Best Local Similarity 99.4%; Pred. No. 7e-144;
Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 60
DB 2300 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 2241
QY 61 ACAAGGCAAGGCTTCACCGCAATTCATGAAGATCTGTAGGTTAGCGTTTTCGG 120
DB 2240 ACAAGGCAAGGCTTCACCGCAATTCATGAAGATCTGTAGGTTAGCGTTTTCGG 2181
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGACACACGAGTGTCTTTCGG 180
DB 2180 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGACACACGAGTGTCTTTCGG 2121
QY 181 CGAAGACGGGCTTCGCTTGTAGCGGTTAGAGTCCCTCAGGATATAGTCTTCG 240
DB 2120 CGAAGACGGGCTTCGCTTGTAGCGGTTAGAGTCCCTCAGGATATAGTCTTCG 2061
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DB 2060 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 2001
QY 301 TAAAGATGTATGCAATGCTTCAAGGAGAGAAAGCAACCGTGCATGCCGATGG 360
DB 2000 TAAAGATGTATGCAATGCTTCAAGGAGAGAAAGCAACCGTGCATGCCGATGG 1941
QY 361 TGAAGTAAAGTGTACGATCGCTTATAGGAGGCAACAGCGGCTCTGCATGGA 420
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DB 1820 ACAATAAACCCATTGACATTCACCAATTTGGTGTGCACCTC 1777

RESULT 12
SYNRSV3MV
LOCUS Cloning vector RSV3. 3557 bp DNA circular SYN 27-APR-1993
DEFINITION Cloning vector RSV3.
ACCESSION M83240
VERSION M83240.1 GI:209303
KEYWORDS cDNA expression vector.
SOURCE unidentified cloning vector
ORGANISM artificial sequences; vectors.
REFERENCE 1 (sites)
Messing,J.
TITLE New M13 vectors for cloning
JOURNAL Meth. Enzymol. 101, 20-78 (1983)
MEDLINE 83296918
PUBMED 6310323
REFERENCE 2 (sites)
Gorman,C., Padmanabhan,R. and Howard,B.H.
TITLE High efficiency DNA-mediated transformation of primate cells
JOURNAL Science 221 (4610), 551-553 (1983)
MEDLINE 8349156
PUBMED 6306768
REFERENCE 3 (bases 1 to 3557)
JACOBS,S., SEKALY,R.P., JACOBSON,C.L., MCFARLAND,H.F. and LONG,E.O.
TITLE HLA class II-restricted presentation of cytoplasmic measles virus

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antigens to cytotoxic T cells
JOURNAL J. Virol. 63 (4), 1756-1762 (1989)
MEDLINE 89178963
PUBMED 2784508
COMMENT Original source text: Cloning vector DNA.
FEATURES
source
Location/Qualifiers
1. .3557
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
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1. .29
/function="polylinker"
/evidence=experimental
misc_feature
912. .3029
/function="ampicillin-resistance, replication origin"
/evidence=experimental
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3030. .3557
/standard_name="5'LTR of Rous Sarcoma Virus"
/citation=[2]
/evidence=experimental

ORIGIN
Query Match 96.7%; Score 505.6; DB 12; Length 3557;
Best Local Similarity 99.0%; Pred. No. 6.6e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 60
DB 3030 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 3089
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DB 3150 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGACACACGAGTGTCTTTCGG 3209
QY 181 CGAAGACGGGCTTCGCTTGTAGCGGTTAGAGTCCCTCAGGATATAGTCTTCG 240
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DB 3270 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 3329
QY 301 TAAAGATGTATGCAATGCTTCAAGGAGAGAAAGCAACCGTGCATGCCGATGG 360
DB 3330 TAAAGATGTATGCAATGCTTCAAGGAGAGAAAGCAACCGTGCATGCCGATGG 3389
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DB 3390 TGAAGTAAAGTGTACGATCGCTTATAGGAGGCAACAGCGGCTCTGCATGGA 3449
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DB 3510 ACAATAAACCCATTGACATTCACCAATTTGGTGTGCACCTC 3553

RESULT 13
AR071324/c
LOCUS AR071324
DEFINITION Sequence 2 from patent US 5910488.
ACCESSION AR071324
VERSION AR071324.1 GI:7222212
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 4059)  
AUTHORS Nabel, G.J., Nabel, E.G., Lew, D., and Marquet, M.  
TITLE Plasmids suitable for gene therapy  
JOURNAL Patent: US 5910488-A 2 08-JUN-1999;  
FEATURES Location/Qualifiers  
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Query Match 96.7%; Score 505.6; DB 6; Length 4059;  
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1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
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Db 3355 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTCTTAGGGTTAGCGGTTTTCG 3296  
Qy 121 CTGCTCCGCGATGTACGGCCAGATATTCGCGTATCTGAGGGACTAGGTGTGTTAGG 180  
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Qy 181 CGAAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTTTCGC 240  
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Qy 361 TGGAGTAAGGTGATGATGCTGCTTATTAGAGGAGCAACAGACGGGTCTGACATGA 420  
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Qy 421 TTGGACGAACCACTAAATTCGGATTCGAGAT-ATTGTATTTAGTGGCTAGCTCGAT 479  
Db 2955 TTGGACGAACCACTAAATTCGGATTCGAGAT-ATTGTATTTAGTGGCTAGCTCGAT 2936  
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Db 2935 ACAATAAGCGCATTTGACCATTCACCATTTGCTGTGCACCTC 2892

RESULT 14  
A38214  
LOCUS A38214 4341 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 58 from Patent WO9408008.  
ACCESSION A38214  
VERSION A38214.1 GI:2294819  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 4341)  
AUTHORS Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.  
TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION  
JOURNAL Patent: WO 9408008-A 58 14-APR-1994;  
MEDICAL RES COUNCIL (GB)  
COMMENT Other publication CA 2145064 940414  
Other publication AU 4832493 940426  
Other publication JP 8501699T 960227.  
FEATURES Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
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Db 141 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTCTTAGGGTTAGCGGTTTTCG 200  
Qy 121 CTGCTCCGCGATGTACGGCCAGATATTCGCGTATCTGAGGGGACTAGGTGTGTTAGG 180  
Db 201 CTGCTCCGCGATGTACGGCCAGATATTCGCGTATCTGAGGGGACTAGGTGTGTTAGG 260  
Qy 181 CGAAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTTTCGC 240  
Db 261 CGAAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTTTCGC 320  
Qy 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTTGAGTCTTTCGACATGG 300  
Db 321 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTTGAGTCTTTCGACATGG 380  
Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360  
Db 381 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 440  
Qy 361 TGGAGTAAGGTGATGATGCTGCTTATTAGAGGAGCAACAGACGGGTCTGACATGA 420  
Db 441 TGGAGTAAGGTGATGATGCTGCTTATTAGAGGAGCAACAGACGGGTCTGACATGA 500  
Qy 421 TTGGACGAACCACTAAATTCGGATTCGAGAT-ATTGTATTTAGTGGCTAGCTCGAT 479  
Db 501 TTGGACGAACCACTAAATTCGGATTCGAGAT-ATTGTATTTAGTGGCTAGCTCGAT 560  
Qy 480 ACAATAAGCGCATTTGACCATTCACCATTTGCTGTGCACCTC 523  
Db 561 ACAATAAGCGCATTTGACCATTCACCATTTGCTGTGCACCTC 604

RESULT 15  
AX286570  
LOCUS AX286570 4341 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 1 from Patent WO0179510.  
ACCESSION AX286570  
VERSION AX286570.1 GI:17048664  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Rice, J.H. and Stevenson, F.M.  
TITLE Materials and methods relating to immune responses to fusion proteins  
JOURNAL Patent: WO 0179510-A 1 25-OCT-2001;  
Cancer Research Ventures Limited (GB)  
FEATURES Location/Qualifiers  
source 1..4341  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Vector pVAC1"

## ORIGIN

Query Match 96.7%; Score 505.6; DB 6; Length 4341;  
Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60

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Db      81  CTGCTCCCTGCTTGTGTTGGAGTCTGCTAGTGGCGAGCAAAATTAAGCTACA 140
Qy      61  ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 120
Db      141  ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 200
Qy      121  CTGCTTCGCAATTCAGGCGCAGATATTCGGTATCTTGAGGGGACTAGGTTTGG 180
Db      201  CTGCTTCGCAATTCAGGCGCAGATATTCGGTATCTTGAGGGGACTAGGTTTGG 260
Qy      181  CGAAAGCGGCTTCGGTTGACGGGTTAGGATCCCTCAGATATAGTTTGG 240
Db      261  CGAAAGCGGCTTCGGTTGACGGGTTAGGATCCCTCAGATATAGTTTGG 320
Qy      241  TTTTGCATAGGAGGCGGAAATCTAGTCTTATGCAATCTTGTAGTCTTGCAATGG 300
Db      321  TTTTGCATAGGAGGCGGAAATCTAGTCTTATGCAATCTTGTAGTCTTGCAATGG 380
Qy      301  TAACGATAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 360
Db      381  TAACGATAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 440
Qy      361  TCGAGTATAGTGTGCAATCGCTTATAGGAGGCAACAGCGGCTGCAATGCA 420
Db      441  TCGAGTATAGTGTGCAATCGCTTATAGGAGGCAACAGCGGCTGCAATGCA 500
Qy      421  TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 479
Db      501  TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 560
Qy      480  ACAATAAGCCATTGACATTCACCATTCACCATTCACCATTCACCATTCACCATTC 523
Db      561  ACAATAAGCCATTGACATTCACCATTCACCATTCACCATTCACCATTCACCATTC 604

RESULT 16
SYNRSV5GPT  SYNRSV5GPT  4839 bp  DNA  circular SYN 16-MAR-2000
LOCUS       Cloning vector RSV.5 (gpt).
DEFINITION  M83236
ACCESSION   M83236
VERSION     M83236.1 GI:209304
KEYWORDS    cDNA expression vector.
SOURCE      Cloning vector pUC19
ORGANISM    artificial sequences; vectors.
REFERENCE   1 (bases 1 to 4839)
AUTHORS     Long E.O., Rosen-Bronson S., Kaip, D.R., Malnati, M., Sekaly, R.P. and
            Jaramenada, D.
TITLE       Efficient cDNA expression vectors for stable and transient
            expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL     Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE     92011006
PUBMED      1655683
FEATURES    Location/Qualifiers
            source          1..4839
                        /organism="Cloning vector pUC19"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:31851"
                        /focus
            source          1..29
                        /organism="Cloning vector pUC12"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:83674"
                        /note="HindIII to BamHI fragment of pUC12"
            source          30..872
                        /organism="Simian virus 40"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:10633"
                        /note="Bi-directional SV40 termination and
                        poly-adenylation sequences."
            source          873..1929
                        /organism="Escherichia coli"

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source      /mol_type="genomic DNA"
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            1930..2273
            /organism="Simian virus 40"
            /mol_type="genomic DNA"
            /db_xref="taxon:10633"
            /note="SV40 early promoter and origin of replication."
            2274..4311
            /organism="Cloning vector pBR322"
            /mol_type="genomic DNA"
            /db_xref="taxon:47470"
            /note="Ampicillin resistance gene and origin of replication
            from the vector pBR322."
            4312..4839
            /organism="Rous sarcoma virus"
            /mol_type="genomic DNA"
            /db_xref="taxon:11886"
            /note="5' long terminal repeat."
            1..29
            /function="polylinker"
            /evidence=experimental
            complement (873..1929)
            /product="guanine-hypoxanthine phosphoribosyltransferase"
            /standard_name="gpt"
            /note="gpt gene from E.coli, putative mature peptide -
            contains internal stop codons; putative"
            2274..4311
            /function="ampicillin resistance and origin of
            replication"
            /evidence=experimental

ORIGIN

Query Match 96.7%; Score 505.6; DB 12; Length 4839;
Best Local Similarity 99.0%; Pred. No. 6.6e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy      1  CTGCTCCCTGCTTGTGTTGGAGTCTGCTAGTGGCGAGCAAAATTAAGCTACA 60
Db      4312  CTGCTCCCTGCTTGTGTTGGAGTCTGCTAGTGGCGAGCAAAATTAAGCTACA 4371
Qy      61  ACAAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 120
Db      4372  ACAAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 4431
Qy      121  CTGCTTCGCAATTCAGGCGCAGATATTCGGTATCTTGAGGGGACTAGGTTTGG 180
Db      4432  CTGCTTCGCAATTCAGGCGCAGATATTCGGTATCTTGAGGGGACTAGGTTTGG 4491
Qy      181  CGAAAGCGGCTTCGGTTGACGGGTTAGGATCCCTCAGATATAGTTTGG 240
Db      4492  CGAAAGCGGCTTCGGTTGACGGGTTAGGATCCCTCAGATATAGTTTGG 4551
Qy      241  TTTTGCATAGGAGGCGGAAATCTAGTCTTATGCAATCTTGTAGTCTTGCAATGG 300
Db      4552  TTTTGCATAGGAGGCGGAAATCTAGTCTTATGCAATCTTGTAGTCTTGCAATGG 4611
Qy      301  TAACGATAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 360
Db      4612  TAACGATAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 4671
Qy      361  TCGAGTATAGTGTGCAATCGCTTATAGGAGGCAACAGCGGCTGCAATGCA 420
Db      4672  TCGAGTATAGTGTGCAATCGCTTATAGGAGGCAACAGCGGCTGCAATGCA 4731
Qy      421  TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 479
Db      4732  TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 4791
Qy      480  ACAATAAGCCATTGACATTCACCATTCACCATTCACCATTCACCATTCACCATTC 523
Db      4792  ACAATAAGCCATTGACATTCACCATTCACCATTCACCATTCACCATTCACCATTC 4835

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RESULT 17
SYNRSV5NEO
LOCUS SYNRSV5NEO 5108 bp DNA linear SYN 06-APR-2001
DEFINITION cDNA expression vector RSV.5 (neo).
ACCESSION M83237.1
VERSION M83237.1 GI:209305
KEYWORDS cDNA expression vector.
SOURCE Expression vector RSV.5 (neo)
ORGANISM Expression vector RSV.5 (neo)
REFERENCE 1 (bases 1 to 5108)
AUTHORS Long,E.C., Rosen-Bronson,S., Karp,D.R., Malnati,M., Sekaly,R.P. and Jaraquemada,D.
TITLE Efficient cDNA expression vectors for stable and transient expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE 92011006
PUBMED 1655683
FEATURES
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            /organism="Expression vector RSV.5 (neo)"
            /mol_type="genomic DNA"
            /db_xref="taxon:118308"
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                1..29
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:45196"
                    /note="HindIII to BamHI fragment of pUC12."
                30..872
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:10633"
                    /note="Bi-directional SV40 termination and poly-adenylation sequence."
                873..879
                    /organism="unidentified cloning vector"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:45196"
                    /note="Remnant of gpt gene from the cDNA expression vector RSV.5 (gpt)."
                880..2197
                    /organism="Cloning vector pSV2neo"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:31846"
                    /note="TN5 neomycin-resistance gene from cloning vector pSV2neo."
                2198..2542
                    /organism="Simian virus 40"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:10633"
                    /note="SV40 early promoter and origin of replication."
                2543..4580
                    /organism="Cloning vector pBR322"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:47470"
                    /note="Ampicillin resistance gene and origin of replication from pBR322."
            4581..5108
                /organism="Rous sarcoma virus"
                /mol_type="genomic DNA"
                /db_xref="taxon:11886"
                /note="5' long terminal repeat of Rous Sarcoma virus."
            1..29
                /function="polylinker"
            /evidence="experimental"
            complement(880..2197)
                /note="neomycin resistance gene from pSV2neo, putative mature peptide - contains internal stop codons; putative"
            2543..4580
                /product="ampicillin resistance"
                /function="ampicillin resistance and origin of replication"

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/evidence="experimental"
4581..5108
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/function="promoter"
/evidence="experimental"

ORIGIN
Query Match 96.7%; Score 505.6; DB 12; Length 5108;
Best Local Similarity 99.0%; Pred. No. 6.6e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTGCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60
Db 4581 CTGCTCCCTGCTGTGTGTGGAGGTGCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 4640
Qy 61 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGGGCTTTGGC 120
Db 4641 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGGGCTTTGGC 4700
Qy 121 CTGCTTCGGGATGTACGGGCGAGATATTCGGGTATCTGAGGGACTAGGGTGTGTTAGG 180
Db 4701 CTGCTTCGGGATGTACGGGCGAGATATTCGGGTATCTGAGGGACTAGGGTGTGTTAGG 4760
Qy 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240
Db 4761 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 4820
Qy 241 TTTTGCATAGGGGAGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300
Db 4821 TTTTGCATAGGGGAGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 4880
Qy 301 TAACGATGATTTAGCAACATGCCCTTACAAGGAGAGAAAAAGCACCGTCGCGATTGG 360
Db 4881 TAACGATGATTTAGCAACATGCCCTTACAAGGAGAGAAAAAGCACCGTCGCGATTGG 4940
Qy 361 TGGAGTAAAGGTGGTACATCGTGCCTTATTTAGGAGGCAACAGAGGGTGTGACATGGA 420
Db 4941 TGGAGTAAAGGTGGTACATCGTGCCTTATTTAGGAGGCAACAGAGGGTGTGACATGGA 5000
Qy 421 TTGGAGGACACCACTTAATTCGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
Db 5001 TTGGAGGACACCACTTAATTCGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 5060
Qy 480 ACAATAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 523
Db 5061 ACAATAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 5104

RESULT 18
SYNRCRC
LOCUS SYNRCRC 5564 bp DNA linear SYN 27-SEP-1994
DEFINITION Cloning vector murine T-cell receptor C-beta 1 DNA, 3' end of cds.
ACCESSION L36565
VERSION L36565.1 GI:550523
KEYWORDS T-cell receptor C-beta 1; T-cell receptor V-beta; cloning vector.
SOURCE unidentified cloning vector
ORGANISM unidentified cloning vector
REFERENCE 1 (bases 1 to 5564)
AUTHORS Palmer,M.S., Bentley,A., Gould,K. and Townsend,A.R.
TITLE The T cell receptor from an influenza-A specific murine CTL clone
JOURNAL Nucleic Acids Res. 17 (6), 2353 (1989)
MEDLINE 89202046
PUBMED 2784852
REFERENCE 2 (bases 1 to 5564)
AUTHORS Long,E.O., Rosen-Bronson,S., Karp,D.R., Malnati,M., Sekaly,R.P. and Jaraquemada,D.
TITLE Efficient cDNA expression vectors for stable and transient expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE 92011006
PUBMED 1655683
REFERENCE 3 (bases 1 to 5564)

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AUTHORS Denis, F., Soudeyrs, H., Ringette, N. and Sekaly, R.-P.  
 TITLE A simple method for the cloning and functional expression of human T cell receptor Vbeta segments in murine hybridomas  
 JOURNAL Unpublished (1994)  
 COMMENT Original source text: Cloning vector DNA.  
 FEATURES Location/Qualifiers  
 source 1..5564  
 /organism="unidentified cloning vector"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:45196"

CDS  
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 /codon\_start=1  
 /evidence=experimental  
 /transl\_table=11  
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 /protein\_id="AA02448.1"  
 /db\_xref="GI:550524"  
 /translation="VDIAKQKATLVCLAGFFPDHVELSWYNGKEVHGVSTDPQA  
 YKSNYSYCLSSRLRYSATFWHPRNHFRCQVPHGLSEEDKWPESGPKVPTQISAE  
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ORIGIN

Query Match 96.7%; Score 505.6; DB 12; Length 5564;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 DB 5037 CTGCTCCCTGCTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 5096  
 DB 5097 ACAGGCAAGGCTGACCGACAAATTCGATGAAGAATCTGCTAGGGTTAGCGGTTTGG 5156  
 QY 61 ACAGGCAAGGCTGACCGACAAATTCGATGAAGAATCTGCTAGGGTTAGCGGTTTGG 120  
 DB 121 CTGCTTCGGATGATACCGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTTAGG 180  
 DB 5157 CTGCTTCGGATGATACCGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTTAGG 5216  
 QY 181 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGTTCCG 240  
 DB 5217 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGTTCCG 5276  
 QY 241 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATCTTGTAGTCTTGTGCAACATGG 300  
 DB 5277 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATCTTGTAGTCTTGTGCAACATGG 5336  
 QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACGCTGCATGCGATTGG 360  
 DB 5337 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACGCTGCATGCGATTGG 5396  
 QY 361 TGGAGTAAAGTGGTACGATGCTGCTTATTAGGAGGCAACAGACGGGCTCTGACATGGA 420  
 DB 5397 TGGAGTAAAGTGGTACGATGCTGCTTATTAGGAGGCAACAGACGGGCTCTGACATGGA 5456  
 QY 421 TTGAGCAACACCACTAAATTCGGATTCGATGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479  
 DB 5457 TTGAGCAACACCACTAAATTCGGATTCGATGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 5516  
 QY 480 ACATTAACGCCATTTCACCATTTGACCATTTGAGTGTGTCACCTC 523  
 DB 5517 ACATTAACGCCATTTCACCATTTGACCATTTGAGTGTGTCACCTC 5560

RESULT 19  
 LOCUS I56772  
 DEFINITION Sequence 3 from patent US 5650306.  
 ACCESSION I56772  
 VERSION I56772.1 GI:2477185  
 KEYWORDS  
 SOURCE Unknown.

ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1 (bases 1 to 5653)  
 AUTHORS Nabel, G.J., Yang, Z.-Y., Liu, J. and Woffendin, C.  
 TITLE Recombinant nucleic acids for inhibiting HIV gene expression  
 JOURNAL Patent: US 5650306-A 3 22-JUL-1997;  
 FEATURES Location/Qualifiers  
 source 1..5653  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 96.7%; Score 505.6; DB 6; Length 5653;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 DB 81 CTGCTCCCTGCTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 140  
 QY 61 ACAGGCAAGGCTGACCGACAAATTCGATGAAGAATCTGCTAGGGTTAGCGGTTTGG 120  
 DB 141 ACAGGCAAGGCTGACCGACAAATTCGATGAAGAATCTGCTAGGGTTAGCGGTTTGG 200  
 QY 121 CTGCTTCGGATGATACCGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTTAGG 180  
 DB 201 CTGCTTCGGATGATACCGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTTAGG 260  
 QY 181 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGTTCCG 240  
 DB 261 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGTTCCG 320  
 QY 241 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATCTTGTAGTCTTGTGCAACATGG 300  
 DB 321 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATCTTGTAGTCTTGTGCAACATGG 380  
 QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACGCTGCATGCGATTGG 360  
 DB 381 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACGCTGCATGCGATTGG 440  
 QY 361 TGGAGTAAAGTGGTACGATGCTGCTTATTAGGAGGCAACAGACGGGCTCTGACATGGA 420  
 DB 441 TGGAGTAAAGTGGTACGATGCTGCTTATTAGGAGGCAACAGACGGGCTCTGACATGGA 500  
 QY 421 TTGAGCAACACCACTAAATTCGGATTCGATGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479  
 DB 501 TTGAGCAACACCACTAAATTCGGATTCGATGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 560  
 QY 480 ACATTAACGCCATTTCACCATTTGACCATTTGAGTGTGTCACCTC 523  
 DB 561 ACATTAACGCCATTTCACCATTTGAGTGTGTCACCTC 604

RESULT 20  
 LOCUS I95540  
 DEFINITION Sequence 1 from patent US 5733543.  
 ACCESSION I95540  
 VERSION I95540.1 GI:3940010  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1 (bases 1 to 5653)  
 AUTHORS Nabel, G.J., Woffendin, C., Yang, N.-S. and Sheehy, M.J.  
 TITLE Introduction of HIV-protective genes into cells by particle-mediated gene transfer  
 JOURNAL Patent: US 5733543-A 1 31-MAR-1998;  
 FEATURES Location/Qualifiers  
 source 1..5653  
 /organism="unknown"  
 /mol\_type="unassigned DNA"



Query Match 96.7%; Score 505.6; DB 6; Length 5653;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTGTGTGGAGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 140

Qy 51 ACAAGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 200

Qy 121 CTGCTTCGCGATGTACGGGCGACATATCGCGTCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 201 CTGCTTCGCGATGTACGGGCGACATATCGCGTCTGAGGGGACTAGGGTGTGTTAGG 260

Qy 191 CGAAAAGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGATTTCGC 240  
 Db 251 CGAAAAGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGATTTCGC 320

Qy 241 TTTTGCATAGCGAGGGGAATGAGTCTTATGCACTCTTGTAGTCTTGCACATGG 300  
 Db 321 TTTTGCATAGCGAGGGGAATGAGTCTTATGCACTCTTGTAGTCTTGCACATGG 380

Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGACCGTGCATGCCGATTGG 360  
 Db 381 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGACCGTGCATGCCGATTGG 440

Qy 361 TGGAGTAAGGTTGAGTACGTCGCTTATAGGAAGCAACAGCGGTTCTGACATGA 420  
 Db 441 TGGAGTAAGGTTGAGTACGTCGCTTATAGGAAGCAACAGCGGTTCTGACATGA 500

Qy 421 TTGAGCAACCACTAATTCGCGATTCGAGAGAT-ATTGTATTATAGTGCCTAGCTCGAT 479  
 Db 501 TTGAGCAACCACTAATTCGCGATTCGAGAGAT-ATTGTATTATAGTGCCTAGCTCGAT 560

Qy 480 ACAATAAGCGCATTTGACCATTCACCAATTTGTTGTCACCTC 523  
 Db 561 ACAATAAGCGCATTTGACCATTCACCAATTTGTTGTCACCTC 604

RESULT 21  
 SYNPRSVNeo/c  
 LOCUS SYNPRSVNeo 5736 bp DNA circular SYN 27-APR-1993  
 DEFINITION PRSVNeo cloning vector for high efficiency gene transfer into mammalian cells.  
 ACCESSION M77786  
 VERSION M77786.1 GI:209147  
 SOURCE synthetic construct  
 KEYWORDS artificial sequences.  
 ORGANISM 1 (bases 1 to 5736)  
 REFERENCE Gilbert.W.  
 AUTHORS Obtained from VecBase 3.0  
 JOURNAL Unpublished (1991)  
 COMMENT Original source text: Synthetic construct DNA.  
 These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program. PRSVNeo - Cloning Vector for High Efficiency Gene Transfer into Mammalian Cells  
 ENTRY PRSVNeo #TYPE DNA CIRCULAR TITLE PRSVNeo - Cloning Vector for High Efficiency Gene Transfer into Mammalian Cells  
 DATE 06-JUN-1986  
 #sequence 16-DEC-1986  
 ACCESSION V00064  
 SOURCE artificial  
 COLLECTION ATCC 37198  
 REFERENCE  
 #number 1  
 #authors Gorman C.

#book 'DNA cloning Volume II, a practical approach', pp. 143-190,  
 edited by D. M. Glover, IRL Press, (1986),  
 eds. D. Rickwood and B. D. Hames

COMMENT  
 Entered by William Gilbert, Whitaker College, MIT, 02-APR-1986  
 Revised 16-DEC-1986 by F. Pfeiffer:  
 1012/3 'AT' to 'TA' to match revised sequence of PBR322 KEYWORDS  
 CROSSREFERENCE

#parent  
 VecBase (3): PBR322, GenBank (50): SV40G,  
 GenBank (50): ALRPROLTB,  
 GenBank (50): Trn5Neo, GenBank (50): Trn5IR1

PARENT  
 Features of PRSVNeo (5736 bp)  
 residue source  
 6- 529 550- 27 (c) Rous Sarcoma Virus (GenBank (50):  
 ALRPROLTB)  
 6- 529 3189-2667 (c) GenBank (50): ALRPROLTB (6 mutations)  
 529-2644 2248-4363 pBR322  
 2641-3634 1781-2774 SV40  
 3631-4244 4100-4713 SV40  
 4248-5533 1286- 1 (c) Trn5 (GenBank (50): TRN5NEO)  
 5251-5736 1720-1235 (c) Trn5 (GenBank (50): TRN5IR1)  
 Conflict (cfl) and Mutations (mut): none

FEATURE  
 1579-2367 789-1 (c) Ap-R; b-lactamase  
 4589-5383 791-1 (c) Neo-R

POLYLINKER  
 SELECTION #resistance Ap  
 SUMMARY PRSVNeo #length 5736 #checksum 3569.  
 Location/Qualifiers  
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 /db\_xref="taxon:32630"

ORIGIN  
 Query Match 96.7%; Score 505.6; DB 12; Length 5736;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 60  
 Db 528 CTGCTCCCTGCTGTGTGGAGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 469

Qy 61 ACAAGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 120  
 Db 468 ACAAGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 409

Qy 121 CTGCTTCGCGATGTACGGGCGACATATCGCGTCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 408 CTGCTTCGCGATGTACGGGCGACATATACGCTATCTGAGGGGACTAGGGTGTGTTAGG 349

Qy 181 CGAAAAGCGGGCTTCGGTTGTACGCGGTTAGGATCCCTCAGGATATAGTTTCGC 240  
 Db 348 CGAAAAGCGGGCTTCGGTTGTACGCGGTTAGGATCCCTCAGGATATAGTTTCGC 289

Qy 241 TTTTGCATAGCGAGGGGAATGAGTCTTATGCACTCTTGTAGTCTTGCACATGG 300  
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Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGACCGTGCATGCCGATTGG 360  
 Db 228 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGACCGTGCATGCCGATTGG 169

Qy 361 TGGAGTAAGGTTGAGTACGTCGCTTATAGGAAGCAACAGCGGTTCTGACATGA 420  
 Db 168 TGGAGTAAGGTTGAGTACGTCGCTTATAGGAAGCAACAGCGGTTCTGACATGA 109

Qy 421 TTGAGCAACCACTAATTCGCGATTCGAGAGAT-ATTGTATTATAGTGCCTAGCTCGAT 479  
 Db 108 TTGAGCAACCACTAATTCGCGATTCGAGAGAT-ATTGTATTATAGTGCCTAGCTCGAT 49

QY 480 ACATTAAGCGCATTTGACCATTCACCATTTGGTGGACCTC 523  
 DB 48 ACATTAAGCGCATTTGACCATTCACCATTTGGTGGACCTC 5

RESULT 22  
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 LOCUS Cloning vector pGlaRSV, complete sequence.  
 DEFINITION U19931  
 VERSION U19931.1 GI:644834  
 KEYWORDS  
 SOURCE Cloning vector pGlaRSV  
 ORGANISM Cloning vector pGlaRSV  
 Cloning vector pGlaRSV  
 artificial sequences, vectors.  
 REFERENCE 1 (bases 1 to 6864)  
 AUTHORS Gottgens,B.B.  
 TITLE A versatile lacZ reporter vector  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 641 to 4011)  
 AUTHORS Ravid,K., Beeler,D.L., Rabin,M.S., Ruley,H.E. and Rosenberg,R.D.  
 TITLE Selective targeting of gene products with the megakaryocyte platelet factor 4 promoter  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1521-1525 (1991)  
 MEDLINE 91142205  
 PUBMED 1899930  
 REFERENCE 3 (bases 1 to 6864)  
 AUTHORS Gottgens,B.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JAN-1995) Berthold B. Gottgens, Hematology, Cambridge University, MRC Centre, Hills Road, Cambridge, UK, CB2 2QH  
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 HPLWYLCRVGLYVDEANIEFHGMVPMRLTDDPRLPAMSEVTEMVQRNHP  
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 DRWEPELNEATPDERDITPMVAMATTIRKLTLGELLTLASRQQLIDMADKVGFL  
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 ORIGIN  
 Query Match 96.7%; Score 505.6; DB 12; Length 6864;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTCTGTGTGTGAGGTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60  
 DB 106 CTGCTCCCTCTGTGTGTGAGGTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 165  
 QY 61 ACAAGGCAAGGCTTGACGACAATTCGATGAAGAATCTGCTTAGGGTTAGGGTTTGGC 120  
 DB 166 ACAAGGCAAGGCTTGACGACAATTCGATGAAGAATCTGCTTAGGGTTAGGGTTTGGC 225  
 QY 121 CTGCTTGCAGATGATGCGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 180  
 DB 226 CTGCTTGCAGATGATGCGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 285  
 QY 181 CGAAAAGCGGGGCTTCGGTTGCTAGCGGTTAGGATGCCCTCAGGATATAGTAGTTTCGC 240  
 DB 286 CGAAAAGCGGGGCTTCGGTTGCTAGCGGTTAGGATGCCCTCAGGATATAGTAGTTTCGC 345  
 QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 300  
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 DB 406 TAACGATGATGACCAACATGCTTACAGGAGAGAAAACGCGTGCATGCCATTGG 465  
 QY 361 TGGAAAGTAAGGTGTGATGATGCTTATTTAGGAGGCAACAGACGGGTCTGACATGA 420  
 DB 466 TGGAAAGTAAGGTGTGATGATGCTTATTTAGGAGGCAACAGACGGGTCTGACATGA 525  
 QY 421 TTGAGCGAACCACTAATTCGCGATTGACAGAT-ATTGTATTAAAGTCCTAGCTCGAT 479  
 DB 526 TTGAGCGAACCACTAATTCGCGATTGACAGAT-ATTGTATTAAAGTCCTAGCTCGAT 585  
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RESULT 23  
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 LOCUS 158322 8591 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 6 from patent US 5652092.  
 ACCESSION 158322  
 VERSION 158322.1 GI:2477560  
 KEYWORDS  
 SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5652092-A 6 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
Db 4716 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTGAGTGTGCGGAGCAAAATTTAAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGGCTTTTGG 120  
Db 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGGCTTTTGG 4835

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 4895

QY 181 CGAAAACGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTGTTCGC 240  
Db 4896 CGAAAACGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTGTTCGC 4955

QY 241 TTTTGGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

QY 301 TAAAGATGATTTAGCAATGCTCTTACAGGAGAGAAAGACACCGTGCATCCGATTTGG 360  
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Db 5076 TGGAGTAAGGTGTGATGATCGTCTTATAGGAGGCAACAGCGGTCTGACATGGA 5135

QY 421 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 5136 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 5195

QY 480 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 523  
Db 5196 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 5239

RESULT 25  
LOCUS I60508 8591 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 6 from patent US 5656477.  
ACCESSION I60508  
VERSION I60508.1 GI:2478953  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5656477-A 6 12-AUG-1997;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
Db 4716 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTGAGTGTGCGGAGCAAAATTTAAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGGCTTTTGG 120  
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QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 4895

QY 181 CGAAAACGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTGTTCGC 240  
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Db 4956 TTTTGGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

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QY 361 TGGAGTAAGGTGTGATGATCGTCTTATAGGAGGCAACAGCGGTCTGACATGGA 420  
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QY 421 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 5136 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 5195

QY 480 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 523  
Db 5196 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 5239

RESULT 24  
LOCUS I58323 8591 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 8 from patent US 5652092.  
ACCESSION I58323  
VERSION I58323.1 GI:2477561  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5652092-A 8 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..8591  
/organism="unknown"  
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ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
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QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGGCTTTTGG 120  
Db 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGGCTTTTGG 4835

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 4895

QY 181 CGAAAACGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTGTTCGC 240  
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QY 241 TTTTGGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

QY 301 TAAAGATGATTTAGCAATGCTCTTACAGGAGAGAAAGACACCGTGCATCCGATTTGG 360  
Db 5016 TAAAGATGATTTAGCAATGCTCTTACAGGAGAGAAAGACACCGTGCATCCGATTTGG 5075

QY 361 TGGAGTAAGGTGTGATGATCGTCTTATAGGAGGCAACAGCGGTCTGACATGGA 420  
Db 5076 TGGAGTAAGGTGTGATGATCGTCTTATAGGAGGCAACAGCGGTCTGACATGGA 5135

QY 421 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 5136 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 5195

QY 480 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 523  
Db 5196 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 5239

RESULT 25  
LOCUS I60508 8591 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 6 from patent US 5656477.  
ACCESSION I60508  
VERSION I60508.1 GI:2478953  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5656477-A 6 12-AUG-1997;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
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Db 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGGCTTTTGG 4835

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTGATCTGAGGGGACTAGGGTGTGTTAGG 4895

QY 181 CGAAAACGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTGTTCGC 240  
Db 4896 CGAAAACGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTGTTCGC 4955

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QY 361 TGGAGTAAGGTGTGATGATCGTCTTATAGGAGGCAACAGCGGTCTGACATGGA 420  
Db 5076 TGGAGTAAGGTGTGATGATCGTCTTATAGGAGGCAACAGCGGTCTGACATGGA 5135

QY 421 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 5136 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 5195

QY 480 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 523  
Db 5196 ACAATAAGCCATTGTACCATTCACACATTTGTTGTCACCTC 5239



QY 421 TTGACGACCACTAATTCGCGATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
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 ACCESSION I77053  
 VERSION I77053.1 GI:3013207  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 8591)  
 AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.  
 TITLE Method of detecting amyloid precursor proteins  
 JOURNAL Patent: US 5693478-A 8 02-DEC-1997;  
 FEATURES Location/Qualifiers  
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ORIGIN  
 Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
 Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
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 QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGTTAGGTTAGGCGTTTTCGG 120  
 Db 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGTTAGGTTAGGCGTTTTCGG 4835  
 QY 121 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 180  
 Db 4836 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 4895  
 QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTCGC 240  
 Db 4896 CGAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTCGC 4955  
 QY 241 TTTTGCATAGGAGGAGGGAATAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
 Db 4956 TTTTGCATAGGAGGAGGGAATAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 5015  
 QY 301 TAACGATGATTAGCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 360  
 Db 5016 TAACGATGATTAGCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 5075  
 QY 361 TGGAGTATAGGTGTGATCGATCGCTTATAGAGGAGGAAAGACCGTGCATGCCGATTGG 420  
 Db 5076 TGGAGTATAGGTGTGATCGATCGCTTATAGAGGAGGAAAGACCGTGCATGCCGATTGG 5135  
 QY 421 TTGAGCAACCACTAAATTCGCGATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db 5136 TTGAGCAACCACTGAATTCGCGATTCAGAGATATTGTATTAAAGTGCCTAGCTCGAT 5195  
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 Db 5196 ACAATAAAGCCATTGACCAATTCACCAATTCAGTGTGACCTC 5239

RESULT 29  
 I87173  
 LOCUS  
 DEFINITION Sequence 8 from patent US 5703209.  
 ACCESSION I87173  
 VERSION I87173.1 GI:3206892  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 8591)  
 AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.  
 TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide

DEFINITION Sequence 6 from patent US 5703209.  
 ACCESSION I87173  
 VERSION I87173.1 GI:3206892  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 8591)  
 AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.  
 TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
 JOURNAL Patent: US 5703209-A 6 30-DEC-1997;  
 FEATURES Location/Qualifiers  
 source 1..8591  
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ORIGIN  
 Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
 Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 Db 4716 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 4775  
 QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGTTAGGTTAGGCGTTTTCGG 120  
 Db 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGTTAGGTTAGGCGTTTTCGG 4835  
 QY 121 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 180  
 Db 4836 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 4895  
 QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTCGC 240  
 Db 4896 CGAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTCGC 4955  
 QY 241 TTTTGCATAGGAGGAGGGAATAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
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 QY 301 TAACGATGATTAGCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 360  
 Db 5016 TAACGATGATTAGCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 5075  
 QY 361 TGGAGTATAGGTGTGATCGATCGCTTATAGAGGAGGAAAGACCGTGCATGCCGATTGG 420  
 Db 5076 TGGAGTATAGGTGTGATCGATCGCTTATAGAGGAGGAAAGACCGTGCATGCCGATTGG 5135  
 QY 421 TTGAGCAACCACTAAATTCGCGATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db 5136 TTGAGCAACCACTGAATTCGCGATTCAGAGATATTGTATTAAAGTGCCTAGCTCGAT 5195  
 QY 480 ACAATAAAGCCATTGACCAATTCACCAATTCAGTGTGACCTC 523  
 Db 5196 ACAATAAAGCCATTGACCAATTCACCAATTCAGTGTGACCTC 5239

RESULT 30  
 I87174  
 LOCUS  
 DEFINITION Sequence 8 from patent US 5703209.  
 ACCESSION I87174  
 VERSION I87174.1 GI:3206892  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 8591)  
 AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.  
 TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide

JOURNAL Patent: US 5703209-A 8 30-DEC-1997;

# FEATURES

source  
Location/Qualifiers  
1. .8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGGC 120  
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGGC 4835

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTGG 180  
DB 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTGG 4895

QY 181 CGAAAGCGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
DB 4896 CGAAAGCGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 4955

QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 4956 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

QY 301 TAAACATGAGTTAGCAACATGCTCTTACAGGAGAGAAAGACCTGTCATGCCGATTGG 360  
DB 5016 TAAACATGAGTTAGCAACATGCTCTTACAGGAGAGAAAGACCTGTCATGCCGATTGG 5075

QY 361 TGAAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 420  
DB 5076 TGAAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 5135

QY 421 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 479  
DB 5136 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 5195

QY 480 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 523  
DB 5196 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 5239

## RESULT 31

XXU02428 10737 bp DNA circular SYN 29-JAN-1997  
LOCUS Cloning vector pBR2, complete sequence.  
DEFINITION U02428  
ACCESSION U02428  
VERSION U02428.1 GI:413794  
KEYWORDS Cloning vector pBR2  
SOURCE Cloning vector pBR2  
ORGANISM artificial sequences; vectors.

## REFERENCE

1. (bases 1 to 10737)  
Murphy,A.J., Kung,A.H., Swirski,R.A. and Schimke,R.T.  
cDNA expression cloning in human cells using the plambdadr2  
episomal vector system  
Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)

## JOURNAL

REFERENCE 2 (bases 1 to 10737)  
Kitts,P.A.  
AUTHORS ClONTECH Vectors On Disc version 1.3  
TITLE Unpublished  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 10737)  
Kitts,P.A.  
AUTHORS Direct Submission  
TITLE Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,  
1020 East Meadow Circle, Palo Alto, CA 94303, USA  
JOURNAL This vector can be obtained from CLONTECH Laboratories, Inc., 1020

East Meadow Circle, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424- 8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH; this vector has not been completely sequenced. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM..

## FEATURES

source  
Location/Qualifiers  
1. .10737  
/organism="Cloning vector pBR2"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31805"

## ORIGIN

Query Match 96.7%; Score 505.6; DB 12; Length 10737;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
DB 148 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 207

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGGC 120  
DB 208 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGGC 267

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTGG 180  
DB 268 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTGG 327

QY 181 CGAAAGCGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
DB 328 CGAAAGCGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 387

QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTCCACATGG 300  
DB 388 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTCCACATGG 447

QY 301 TAAACATGAGTTAGCAACATGCTCTTACAGGAGAGAAAGACCTGTCATGCCGATTGG 360  
DB 448 TAAACATGAGTTAGCAACATGCTCTTACAGGAGAGAAAGACCTGTCATGCCGATTGG 507

QY 361 TGAAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 420  
DB 508 TGAAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 567

QY 421 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 479  
DB 568 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 627

QY 480 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 523  
DB 628 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 671

## RESULT 32

U02455 10850 bp DNA circular SYN 29-MAR-1996  
LOCUS Cloning vector rpBR2, complete sequence.  
DEFINITION U02455  
ACCESSION U02455  
VERSION U02455.1 GI:413821  
KEYWORDS Cloning vector rpBR2  
SOURCE Cloning vector rpBR2  
ORGANISM artificial sequences; vectors.  
REFERENCE 1 (bases 1 to 10850)  
Kitts,P.A.  
AUTHORS CLONTECH Vectors On Disc version 1.3  
TITLE Unpublished  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 10850)  
 AUTHORS Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.  
 TITLE cDNA expression cloning in human cells using the plambdaDR2  
 JOURNAL episomal vector system  
 REFERENCE Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)  
 AUTHORS Kitts,P.A.  
 JOURNAL Direct Submission  
 TITLE Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,  
 COMMENT 1020 East Meadow Circle, Palo Alto, CA 94303, USA  
 East Meadow Circle, Palo Alto, CA 94303, USA. To place an order  
 call (415) 424-8222 or (800) 662-2566, extension 1. International  
 customers, please contact your local distributor. For technical  
 information, call (415) 424- 8222 or (800) 662-2566, extension 3.  
 This sequence was compiled by Andrew Murphy and revised at  
 CLONTECH. If you suspect there is an error in this sequence, please  
 contact CLONTECH's technical service department at (415) 424-8222  
 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.

FEATURES  
 source  
 1..10850  
 /organism="Cloning vector rpDR2"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:31858"  
 /note="Plasmid released from lambda DR2"

ORIGIN  
 Query Match 96.7%; Score 505.6; DB 12; Length 10850;  
 Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGTACA 60  
 148 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGTACA 207  
 61 ACAAGCAGAGGCTGACCGACATTCATGAGATTCGCTAGGTTAGCGTTTTCGG 120  
 208 ACAAGCAGAGGCTGACCGACATTCATGAGATTCGCTAGGTTAGCGTTTTCGG 267  
 121 CTGCTCCGATGATGACGGCGCAGATTCGCGTATCTGAGGGGACTAGGTTGTTAGG 180  
 268 CTGCTCCGATGATGACGGCGCAGATTCGCGTATCTGAGGGGACTAGGTTGTTAGG 327  
 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTTCG 240  
 328 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTTCG 387  
 241 TTTTGCATAGGGGGGGAATGTAGTCTTATGCAATCTCTGAGTCTTGCACATGG 300  
 388 TTTTGCATAGGGGGGGAATGTAGTCTTATGCAATCTCTGAGTCTTGCACATGG 447  
 301 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAAGCACCGTGATGCGGATTGG 360  
 448 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAAGCACCGTGATGCGGATTGG 507  
 361 TGAAGTATAGTGTGATGATGCTGCTTATAGAGAGGCAACAGACGGTCTGACATGA 420  
 508 TGAAGTATAGTGTGATGATGCTGCTTATAGAGAGGCAACAGACGGTCTGACATGA 567  
 421 TTGAGCAGACCACTAATTCGCAATTCGAGAGAT-ATTGTATTTAGTGGCTAGCTCGAT 479  
 568 TTGAGCAGACCACTAATTCGCAATTCGAGAGAT-ATTGTATTTAGTGGCTAGCTCGAT 627  
 480 ACAATAAGCGCATTTGACCATTCACCACTTGGTGTGCACCTC 523  
 628 ACAATAAGCGCATTTGACCATTCACCACTTGGTGTGCACCTC 671

RESULT 33  
 ALRPROLTB  
 LOCUS 633 bp ss-RNA linear VRL 28-APR-1993  
 DEFINITION Rous sarcoma virus (Schmidt-Ruppin), proviral, 3' LTR on 21S mRNA.  
 ACCESSION J02025

J02025.1 GI:210255  
 c-myc proto-oncogene; long terminal repeat (LTR); src oncogene.  
 Rous sarcoma virus  
 ORGANISM Rous sarcoma virus  
 REFERENCE 1 (sites)  
 AUTHORS Yamamoto,T., de Crombrughe,B. and Pastan,I.  
 TITLE Identification of a functional promoter in the long terminal repeat  
 JOURNAL Cell 22 (3), 787-797 (1980)  
 MEDLINE 81112147  
 PUBMED 6257399  
 REFERENCE 2 (bases 1 to 633)  
 AUTHORS Yamamoto,T., Tyagi,J.S., Pagan,J.B., Jay,G., deCrombrughe,B. and  
 Pastan,I.  
 TITLE Molecular mechanism for the capture and excision of the  
 transforming gene of avian sarcoma virus as suggested by analysis  
 of recombinant clones  
 JOURNAL J. Virol. 35 (2), 436-443 (1980)  
 MEDLINE 81072438  
 PUBMED 6255184  
 REFERENCE 3 (bases 319 to 633)  
 AUTHORS Yamamoto,T., Jay,G. and Pastan,I.  
 TITLE Unusual features in the nucleotide sequence of a cDNA clone derived  
 from the common region of avian sarcoma virus messenger RNA  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (1), 176-180 (1980)  
 MEDLINE 80145590  
 PUBMED 6244542  
 COMMENT Original source text: Rous sarcoma virus (Schmidt-Ruppin strain,  
 subgroup D) provirus, cDNA to 21S mRNA from infected chicken  
 embryonic fibroblasts, clone pSR1.  
 [1] sites; mRNA start.  
 Original figure in [2] included 24 'g's on 5' end and 16 'c's on 3'  
 end that were cDNA synthesis artifacts.  
 [2] also sequenced a defective clone, pSR2, with the src gene  
 deleted (see separate entry).  
 [1] demonstrated the mRNA transcription initiation site shown in  
 the Sites table using pSR1 as a template. However, this is the 3'  
 LTR, and the functional mRNA start site would be assumed to be on  
 the 5' LTR at the homologous site.

FEATURES  
 source  
 1..633  
 /organism="Rous sarcoma virus"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:11886"  
 <1..517  
 /note="viral genomic RNA"  
 211..5633  
 /note="3' LTR"  
 517..5633  
 /note="in vitro mRNA [1]; see comment"  
 repeat\_region 517..536  
 /note="terminally redundant repeat"  
 ORIGIN 20 bp upstream of pET1 site.

Query Match 96.5%; Score 504.6; DB 14; Length 633;  
 Best Local Similarity 99.0%; Pred. No. 1.3e-142;  
 Matches 518; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60  
 28 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 87  
 61 ACAAGCAGAGGCTTGACCGACAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTTCGG 120  
 88 ACAAGCAGAGGCTTGACCGACAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTTCGG 147  
 121 CTGCTTCGCGATGTACCGGCCAGATATTCGCGGTATCTGAGGGGACTAGCGTTTCGAG 180  
 148 CTGCTTCGCGATGTACCGGCCAGATATTCGCGGTATCTGAGGGGACTAGCGTTTCGAG 207  
 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTTCG 240



Db 208 CGAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 267  
Qy 241 TTTTGCATAGGAGGGGAATAGTCTTATGCAATCTCTGTAGTCTTGCAATGG 300  
Db 268 TTTTGCATAGGAGGGGAATAGTCTTATGCAATCTCTGTAGTCTTGCAATGG 327  
Qy 301 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAGCAACCGTGCATGCGATGG 360  
Db 328 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAGCAACCGTGCATGCGATGG 387  
Qy 361 TGGAGTAGGTTGATGATGCGCTTATAGGAGGCAACAGCGGCTTGACATGA 420  
Db 388 TGGAGTAGGTTGATGATGCGCTTATAGGAGGCAACAGCGGCTTGACATGA 447  
Qy 421 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 448 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 507  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCT 522  
Db 508 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCT 550

RESULT 34  
AR215114  
LOCUS AR215114 6836 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 18 from patent US 6410266.  
ACCESSION AR215114  
VERSION AR215114.1 GI:23313242  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 6836)  
AUTHORS Harrington,J.J. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..6836  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1358  
Qy 61 ACAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 120  
Db 1359 ACAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 1418  
Qy 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGGTGTGTTAGG 180  
Db 1419 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGGTGTGTTAGG 1478  
Qy 181 CGAAAGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240  
Db 1479 CGCCACGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 1538  
Qy 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1598  
Qy 301 TAAAGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 360  
Db 1419 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGGTGTGTTAGG 1478  
Qy 181 CGAAAGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240  
Db 1479 CGCCACGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 1538  
Qy 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1598  
Qy 301 TAAAGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 360  
Db 1599 TAAAGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 1658  
Qy 361 TGGAGTAGGTTGATGATGCGCTTATAGGAGGCAACAGCGGCTTGACATGA 420

Db 1659 TGGAGTAGGTTGATGATGCGCTTATAGGAGGCAACAGCGGCTTGACATGA 1718  
Qy 421 TTTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1719 TTTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1778  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1779 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822

RESULT 35  
AR302356  
LOCUS AR302356 6836 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 18 from patent US 6541221.  
ACCESSION AR302356  
VERSION AR302356.1 GI:31690610  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 6836)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 18 01-APR-2003;  
FEATURES Location/Qualifiers  
source 1..6836  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1358  
Qy 61 ACAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 120  
Db 1359 ACAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 1418  
Qy 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGGTGTGTTAGG 180  
Db 1419 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGGTGTGTTAGG 1478  
Qy 181 CGAAAGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240  
Db 1479 CGCCACGCGGGCTTCGGTTGTACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 1538  
Qy 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1598  
Qy 301 TAAAGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 360  
Db 1599 TAAAGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 1658  
Qy 361 TGGAGTAGGTTGATGATGCGCTTATAGGAGGCAACAGCGGCTTGACATGA 420  
Db 1659 TGGAGTAGGTTGATGATGCGCTTATAGGAGGCAACAGCGGCTTGACATGA 1718  
Qy 421 TTTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1719 TTTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1778  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1779 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822



RESULT 36  
 AR373228  
 LOCUS AR373228 6836 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 18 from patent US 6602686.  
 ACCESSION AR373228  
 VERSION AR373228.1 GI:40075236  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 6836)  
 AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
 TITLE Compositions and method for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6602686-A 18 05-AUG-2003;  
 FEATURES Location/Qualifiers  
 source 1..6836  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAGCAAAATTTAAGCTACA 60  
 1299 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAGCAAAATTTAAGCTACA 1358  
 61 ACAAGGCAAGGCTTGCACGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTTCGG 120  
 1359 ACAAGGCAAGGCTTGCACGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTTCGG 1418  
 121 CTGCTTCGCGATGTAACGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTAGG 180  
 1419 CTGCTTCGCGATGTAACGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTAGG 1478  
 181 CGAAAGCGGGGCTTCGCTGCTACGGGTTAGGAGTCCCTCAGGATATAGTATTTTCG 240  
 1479 CGCCAGCGGGGCTTCGCTGCTACGGGTTAGGAGTCCCTCAGGATATAGTATTTTCG 1538  
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 1539 TTTTGCATAGGAGGGGAAATGTAAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 1598  
 301 TAACGATGATGTAACGATCGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 360  
 1599 TAACGATGATGTAACGATCGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 1658  
 361 TGGAGTAAAGTGGTACGATCGCTTATGCAATACCTCTTGTAGTCTTGCACATGG 420  
 1659 TGGAGTAAAGTGGTACGATCGCTTATGCAATACCTCTTGTAGTCTTGCACATGG 1718  
 421 TTGAGCAACCACTAAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAAT 479  
 1719 TTGAGCAACCACTAAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAAT 1778  
 480 ACAATAAACGCCATTTGACCAATTCACCAATTTGATTTAAGTGCCTAGCTCGAT 523  
 1779 ACAATAAACGCCATTTGACCAATTCACCAATTTGATTTAAGTGCCTAGCTCGAT 1822

RESULT 37  
 AR401614  
 LOCUS AR401614 6836 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 18 from patent US 6623958.  
 ACCESSION AR401614  
 VERSION AR401614.1 GI:40149062  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 6836)  
 AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
 TITLE Compositions and methods for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6623958-A 18 23-SEP-2003;  
 FEATURES Location/Qualifiers  
 source 1..6836  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAGCAAAATTTAAGCTACA 60  
 1299 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAGCAAAATTTAAGCTACA 1358  
 61 ACAAGGCAAGGCTTGCACGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTTCGG 120  
 1359 ACAAGGCAAGGCTTGCACGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTTCGG 1418  
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 1719 TTGAGCAACCACTAAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAAT 1778  
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RESULT 38  
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 LOCUS AF346624 6836 bp DNA circular SYN 30-AUG-2001  
 DEFINITION RAGE vector pRIG1, complete sequence.  
 ACCESSION AF346624  
 VERSION AF346624.1 GI:15383987  
 KEYWORDS  
 SOURCE RAGE vector pRIG1  
 ORGANISM RAGE vector pRIG1  
 artificial sequences; vectors.  
 1 (bases 1 to 6836)  
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,  
 Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boorer,S.,  
 Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,  
 Offenbacher,J., Danzig,J. and Ducar,M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)  
 JOURNAL 21227151  
 MEDLINE 11329013  
 PUBMED

REFERENCE 2 (bases 1 to 6836)  
 AUTHORS Harrington,J.J., Sheriff,B., Rundlett,S., Jackson,P.D., Perry,R.,  
 Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,  
 Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,  
 Veloso,N., Hess,J., Cochran,K., Io,K., Offenbacher,J., Danzig,J.,  
 and Ducat,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-FEB-2001) Athersys, Inc., 3201 Carnegie Ave.,  
 Cleveland, OH 44115, USA  
 FEATURES  
 source 1. 6836  
 Location/Qualifiers  
 /organism="RAGE vector pRIG1"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:161236"  
 ORIGIN  
 Query Match 95.8%; Score 500.8; DB 12; Length 6836;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
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 QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTAAGCTACA 120  
 DB 1359 ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTAAGCTACA 1418  
 QY 121 CTGCTCCGATGTACGGGCGAGATATCGGCTATCTGAGGGACTAGGGTGTGTTAGG 180  
 DB 1419 CTGCTCCGATGTACGGGCGAGATATCGGCTATCTGAGGGACTAGGGTGTGTTAGG 1478  
 QY 181 CGAAAGCGGGCTTCGGTGTGACGGTGTAGTGTGCGGAGCAAAATTAAGCTACA 240  
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 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 300  
 DB 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 1598  
 QY 301 TAACGATGAGTGTACCAATGCTTACAGGAGCAAAAGCAACCGTGTGCGGATGG 360  
 DB 1599 TAACGATGAGTGTACCAATGCTTACAGGAGCAAAAGCAACCGTGTGCGGATGG 1658  
 QY 361 TGGAGTAAAGTGTGACGATCGTGTGCTTATAGGAGGCAACAGCGGCTCTGACATGGA 420  
 DB 1659 TGGAGTAAAGTGTGACGATCGTGTGCTTATAGGAGGCAACAGCGGCTCTGACATGGA 1718  
 QY 421 TTGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGTGCTAGTCTGAT 479  
 DB 1719 TTGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGTGCTAGTCTGAT 1778  
 QY 480 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGACCTC 523  
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 LOCUS AR215118 9737 bp DNA linear PAT 25-SEP-2002  
 DEFINITION Sequence 22 from patent US 6410266.  
 ACCESSION AR215118  
 VERSION AR215118.1 GI:23313246  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 9737)  
 AUTHORS Harrington,J.J. and Rundlett,S.  
 TITLE Compositions and methods for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6410266-A 22 25-JUN-2002;  
 FEATURES  
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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 ORIGIN  
 Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGTAGTGTGCGGAGCAAAATTAAGCTACA 60  
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 QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTAAGCTACA 120  
 DB 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTAAGCTACA 1271  
 QY 121 CTGCTCCGATGTACGGGCGAGATATCGGCTATCTGAGGGACTAGGGTGTGTTAGG 180  
 DB 1272 CTGCTCCGATGTACGGGCGAGATATCGGCTATCTGAGGGACTAGGGTGTGTTAGG 1331  
 QY 181 CGAAAGCGGGCTTCGGTGTGACGGTGTAGTGTGCGGAGCAAAATTAAGCTACA 240  
 DB 1332 CGCCAGCGGGCTTCGGTGTGACGGTGTAGTGTGCGGAGCAAAATTAAGCTACA 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 300  
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 QY 301 TAACGATGAGTGTACCAATGCTTACAGGAGCAAAAGCAACCGTGTGCGGATGG 360  
 DB 1452 TAACGATGAGTGTACCAATGCTTACAGGAGCAAAAGCAACCGTGTGCGGATGG 1511  
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 DB 1512 TGGAGTAAAGTGTGACGATCGTGTGCTTATAGGAGGCAACAGCGGCTCTGACATGGA 1571  
 QY 421 TTGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGTGCTAGTCTGAT 479  
 DB 1572 TTGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGTGCTAGTCTGAT 1631  
 QY 480 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGACCTC 523  
 DB 1632 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGACCTC 1675  
 RESULT 40  
 AR215119  
 LOCUS AR215119 9737 bp DNA linear PAT 25-SEP-2002  
 DEFINITION Sequence 23 from patent US 6410266.  
 ACCESSION AR215119  
 VERSION AR215119.1 GI:23313247  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 9737)  
 AUTHORS Harrington,J.J. and Rundlett,S.  
 TITLE Compositions and methods for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6410266-A 23 25-JUN-2002;  
 FEATURES  
 source 1. 9737  
 Location/Qualifiers  
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 Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGTAGTGTGCGGAGCAAAATTAAGCTACA 60

Db 1152 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 1211  
Qy 61 ACAAGGCAAGGCTTGACCGCAATTTGCATGAAGAATCTGTTAGGCTTAGGCTTTTGGC 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTTGCATGAAGAATCTGTTAGGCTTAGGCTTTTGGC 1271  
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Qy 241 TTTTGCATAGGGGAGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
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Db 1512 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACGAGCGGTCTGACATGA 1571  
Qy 421 TTGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCTAGCTCGAT 479  
Db 1572 TTGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCTAGCTCGAT 1631  
Qy 480 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 1675

RESULT 41  
AR215124  
LOCUS AR215124 9737 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 28 from patent US 6410266.  
ACCESSION AR215124  
VERSION AR215124.1 GI:23313252  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
Harrington,J.J. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6410266-A 28 25-JUN-2002;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
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Qy 61 ACAAGGCAAGGCTTGACCGCAATTTGCATGAAGAATCTGTTAGGCTTAGGCTTTTGGC 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTTGCATGAAGAATCTGTTAGGCTTAGGCTTTTGGC 1271  
Qy 121 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 180  
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Qy 181 CGAAAGCGGGGCTTCGGTGTGAGCGGTAGGATCCCTCAGGATATAGTTTTCG 240  
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Qy 241 TTTTGCATAGGGGAGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
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Qy 421 TTGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCTAGCTCGAT 479  
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Qy 301 TAAGATGATTAGCAATGCTTCAAGGAGAAAGCAACCGTGATGCCGATGG 360  
Db 1452 TAAGATGATTAGCAATGCTTCAAGGAGAAAGCAACCGTGATGCCGATGG 1511  
Qy 361 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACGAGCGGTCTGACATGA 420  
Db 1512 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACGAGCGGTCTGACATGA 1571  
Qy 421 TTGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCTAGCTCGAT 479  
Db 1572 TTGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCTAGCTCGAT 1631  
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RESULT 42  
AR302360  
LOCUS AR302360 9737 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 22 from patent US 6541221.  
ACCESSION AR302360  
VERSION AR302360.1 GI:31690614  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 22 01-APR-2003;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
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Qy 61 ACAAGGCAAGGCTTGACCGCAATTTGCATGAAGAATCTGTTAGGCTTAGGCTTTTGGC 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTTGCATGAAGAATCTGTTAGGCTTAGGCTTTTGGC 1271  
Qy 121 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 180  
Db 1272 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 1331  
Qy 181 CGAAAGCGGGGCTTCGGTGTGAGCGGTAGGATCCCTCAGGATATAGTTTTCG 240  
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Qy 241 TTTTGCATAGGGGAGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
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421 TTGAGCAACCACTAAATTCGGATTGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
1572 TTGAGCAACCACTAAATTCGGATTGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631

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1632 ACAATAAGCCATTGACCAATTCACCACTTTGGTGTGCACCTC 1675

RESULT 43  
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LOCUS AR302361 9737 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 23 from patent US 6541221.  
ACCESSION AR302361  
VERSION AR302361.1 GI:31690615  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 23 01-APR-2003;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
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Patent: US 6541221-A 23 01-APR-2003;  
Location/Qualifiers  
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1212 ACAAGGCAAGGTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTTCG 1271

121 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 180  
1272 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 1331

181 CGAAGGCAAGGTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTTCG 240  
1332 CGAAGGCAAGGTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTTCG 1391

241 TTTTGCATAGGAGGAGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
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1452 TAAAGGTAAGTGTAGCAATCGCTTACAGGAGAGAAAGACCGGTGATCGCGATTGG 1511

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1512 TGAAGTAAGTGTAGCAATCGCTTACAGGAGAGAAAGACCGGTGATCGCGATTGG 1571

421 TTGAGCAACCACTAAATTCGGATTGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
1572 TTGAGCAACCACTAAATTCGGATTGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631

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1632 ACAATAAGCCATTGACCAATTCACCACTTTGGTGTGCACCTC 1675

RESULT 44  
AR302366  
LOCUS AR302366 9737 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 28 from patent US 6541221.  
ACCESSION AR302366  
VERSION AR302366.1 GI:31690620  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 28 01-APR-2003;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Genes  
Patent: US 6541221-A 28 01-APR-2003;  
Location/Qualifiers  
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1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
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61 ACAAGGCAAGGTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTTCG 120  
1212 ACAAGGCAAGGTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTTCG 1271

121 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 180  
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181 CGAAGGCAAGGTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTTCG 240  
1332 CGAAGGCAAGGTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTTCG 1391

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1392 TTTTGCATAGGAGGAGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 1451

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1452 TAAAGGTAAGTGTAGCAATCGCTTACAGGAGAGAAAGACCGGTGATCGCGATTGG 1511

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1512 TGAAGTAAGTGTAGCAATCGCTTACAGGAGAGAAAGACCGGTGATCGCGATTGG 1571

421 TTGAGCAACCACTAAATTCGGATTGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
1572 TTGAGCAACCACTAAATTCGGATTGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631

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RESULT 45  
AR373232  
LOCUS AR373232 9737 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 22 from patent US 6602686.  
ACCESSION AR373232  
VERSION AR373232.1 GI:40075240  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

unclassified.  
 REFERENCE 1 (bases 1 to 9737)  
 AUTHORS Harrington,J., Sherf,B. and Rundlett,S.  
 TITLE Compositions and method for non-targeted activation of endogenous  
 genes  
 JOURNAL Patent: US 6602686-A 23 05-AUG-2003;  
 FEATURES Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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	Query Match	95.8%	Score 500.8	DB 6	Length 9737
	Best Local Similarity	98.5%	Pred. No. 1.9e-141		
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	Gaps	1			
Qy	1	CTGCTCCCTGCTGTGTTGGAGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGTACA	60		
Db	1152	CTGCTCCCTGCTGTGTTGGAGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGTACA	1211		
Qy	61	ACAAGCGAAGCTTGACCGCAAAATTCATGCAAGATCTGCTAGGCTTTAGCGCTTTTGGC	120		

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Db 1272 CTGCTTCGGATGTAGGGGCAAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 1331  
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Db 1572 TTGACAGAACCACTAAATTCGGATTCGAGAT-ATTGTATTTAAAGTCCCTAGCTCGAT 1631  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 48  
AR401618  
LOCUS AR401618 9737 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 22 from patent US 6623958.  
ACCESSION AR401618  
VERSION AR401618.1 GI:40149066  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6623958-A 22 23-SEP-2003;  
FEATURES Location/Qualifiers  
source 1..9737  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTGTGTGTTGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTGTGTGTTGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 1211  
Qy 61 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAAATCTGCTTAGGGTTAGGGTTTTTCGG 120  
Db 1212 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAAATCTGCTTAGGGTTAGGGTTTTTCGG 1271  
Qy 121 CTGCTTCGGATGTAGCGGCAAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
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Qy 181 CGAAAGCGGGCTTCGGTGTGTTAGCGGTTAGGAGTCCCTCAGGATATAGTACTGTTTCG 240  
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Qy 421 TTGACAGAACCACTAAATTCGGATTCGAGAT-ATTGTATTTAAAGTCCCTAGCTCGAT 479  
Db 1572 TTGACAGAACCACTAAATTCGGATTCGAGAT-ATTGTATTTAAAGTCCCTAGCTCGAT 1631  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
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RESULT 49  
AR401619  
LOCUS AR401619 9737 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 23 from patent US 6623958.  
ACCESSION AR401619  
VERSION AR401619.1 GI:40149067  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6623958-A 23 23-SEP-2003;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
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Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTGTGTGTTGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
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Db 1272 CTGCTTCGGATGTAGCGGCAAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 1331  
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Qy 301 TAACGATGATGTAGCAACATGCTTACAAGGAGGAAAGGACCGTSCATGCCGATTGG 360  
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Qy	61	ACAGGCCAAGCCTTGACCAGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTGG	120
Dd	1346	ACAGGCCAAGCCTTGACCAGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTGG	1405
Qy	121	CTGCTTCGGCATGTACGGGCCAGATATTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG	180
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Dd	1586	TAACGATGATTTAGCAACATGCCCTTACAGGAGGAAAAAGCACCGTGATGCGGATTGG	1645
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Qy	421	TTGGACGAACCACTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCTAGCTCGAT	479
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LOCUS	AR401620	9871 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 24 from patent US 6623958.		
ACCESSION	AR401620		
VERSION	AR401620.1 GI:40149068		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 9871)		
TITLE	Harrington,J.J., Sherf,B. and Rundlett,S. Compositions and methods for non-targeted activation of endogenous genes		
JOURNAL	Patent: US 6623958-A 24 23-SEP-2003;		
FEATURES	Location/Qualifiers source 1..9871 /organism="unknown" /mol_type="genomic DNA"		
ORIGIN			
Query Match	95.8%; Score 500.8; DB 6; Length 9871;		
Best Local Similarity	98.5%; Pred. No. 1.9e-141;		
Matches 516; Conservative	0; Mismatches 7; Indels 1; Gaps 1;		
Qy	1	CTGCTCCCTCGTTGTGTGGAGGTCGTGAGTAGTGC CGACGAAATTTAAGCTACA	60
Dd	1286	CTGCTCCCTCGTTGTGTGTGGAGGTCGTGAGTAGTGC CGACGAAATTTAAGCTACA	1345
Qy	61	ACAGGCCAAGCCTTGACCAGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTGG	120
Dd	1346	ACAGGCCAAGCCTTGACCAGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTGG	1405
Qy	121	CTGCTTCGGCATGTACGGGCCAGATATTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG	180



Db 1406 CTGCTTCGGCATGTACGGGCCAGATATACGGGTATCTGAGGGAGCTAGGTGTGTTAGG 1465  
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QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCCTGSCATGCCGATTGG 360  
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Db 1706 TTGGACGAAACCACTAAATTCGCATTCGAGAGATATTTGTATTTAAGTGCCTAGCTCGAT 1765  
QY 480 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACATC 523  
Db 1766 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACATC 1809  
  
RESULT 55  
AR215121  
LOCUS AR215121 10060 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 25 from patent US 6410266.  
ACCESSION AR215121  
VERSION AR215121.1 GI:23313249  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
  
REFERENCE 1 (bases 1 to 10060)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6410266-A 25 25-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..10060  
/organism="unknown"  
/mol\_type="genomic DNA"  
  
ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTCCCTGAGTACTGCGGAGCAAAATTAAGCTACA 60  
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QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 1595 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1654  
QY 181 CGAAAGCGGGCTTCGGTTGTACCGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 1655 CGCCAGCGGGCTTCGGTTGTACCGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 1714  
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Db 1775 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCCTGSCATGCCGATTGG 1834  
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Db 1835 TGGAGTAAAGTGTAGTACGCTGCTTATAGGAGGCAACAGACGGCTTGCATGGA 1894  
QY 421 TTGGACGAAACCACTAAATTCGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1895 TTGGACGAAACCACTAAATTCGCATTCGAGAGATATTTGTATTTAAGTGCCTAGCTCGAT 1954  
QY 480 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACATC 523  
Db 1955 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACATC 1998  
  
RESULT 56  
AR302363  
LOCUS AR302363 10060 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 25 from patent US 6541221.  
ACCESSION AR302363  
VERSION AR302363.1 GI:31690617  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
  
REFERENCE 1 (bases 1 to 10060)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 25 01-APR-2003;  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"  
  
ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTCCCTGAGTACTGCGGAGCAAAATTAAGCTACA 60  
Db 1475 CTGCTCCCTGCTGTGTGTGGAGTCCCTGAGTACTGCGGAGCAAAATTAAGCTACA 1534  
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QY 181 CGAAAGCGGGCTTCGGTTGTACCGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 240  
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QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCCTGSCATGCCGATTGG 360  
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QY 361 TGGAGTAAAGTGTAGTACGCTGCTTATAGGAGGCAACAGACGGCTTGCATGGA 420  
Db 1835 TGGAGTAAAGTGTAGTACGCTGCTTATAGGAGGCAACAGACGGCTTGCATGGA 1894  
QY 421 TTGGACGAAACCACTAAATTCGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1895 TTGGACGAAACCACTAAATTCGCATTCGAGAGATATTTGTATTTAAGTGCCTAGCTCGAT 1954

QY 480 ACAATAAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 523  
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Db 1955 ACAATAAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 1998

RESULT 57  
AR373235  
LOCUS AR373235 10060 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 25 from patent US 6602686.  
ACCESSION AR373235  
VERSION AR373235.1 GI:40075243  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10060)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and method for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6602686-A 25 05-AUG-2003;  
FEATURES  
source Location/Qualifiers  
1..10060  
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ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGTGAAGTGTGCGGAGCAAAATTAAGTACA 60  
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QY 61 ACAGGCAAGGCTTCACCGCAATTCGATGAAGATCTGTTAGGTTAGCGTTTGG 120  
Db 1535 ACAGGCAAGGCTTCACCGCAATTCGATGAAGATCTGTTAGGTTAGCGTTTGG 1594

QY 121 CTGCTCCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGTTGTAGG 180  
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QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 240  
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QY 241 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATACCTTTGAGTCTTGCAACATCG 300  
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QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
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QY 361 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAAGGCAACGAGCGGTTGACATGA 420  
Db 1835 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAAGGCAACGAGCGGTTGACATGA 1894

QY 421 TTGAGCAACCACTAAATTCGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1895 TTGAGCAACCACTAAATTCGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1954

QY 480 ACAATAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 523  
Db 1955 ACAATAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 1998

RESULT 58  
AR401621  
LOCUS AR401621 10060 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 25 from patent US 6623958.  
ACCESSION AR401621  
VERSION AR401621.1 GI:40149069

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10060)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6623958-A 25 23-SEP-2003;  
FEATURES  
source Location/Qualifiers  
1..10060  
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ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGTGAAGTGTGCGGAGCAAAATTAAGTACA 60  
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Db 1535 ACAGGCAAGGCTTCACCGCAATTCGATGAAGATCTGTTAGGTTAGCGTTTGG 1594

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QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
Db 1775 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1834

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Db 1835 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAAGGCAACGAGCGGTTGACATGA 1894

QY 421 TTGAGCAACCACTAAATTCGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1895 TTGAGCAACCACTAAATTCGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1954

QY 480 ACAATAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 523  
Db 1955 ACAATAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 1998

RESULT 59  
AR031159  
LOCUS AR031159 11265 bp DNA circular PAT 20-SEP-2000  
DEFINITION Sequence 1 from Patent WO9844129.  
ACCESSION AR031159  
VERSION AR031159.1 GI:10278512  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Lew,A.M., Boyle,J.S. and Brady,J.L.  
TITLE Enhancement of immune response using targeting molecules  
JOURNAL Patent: WO 9844129-A 1 08-OCT-1998;  
INST MEDICAL W & E HALL (AU) ; QUEENSLAND INST MED RES (AU) ; CSL LTD (AU) ; LEW ANDREW MARK (AU) ; UNIV MELBOURNE (AU) ; BOYLE JEFFREY STEPHEN (AU) ; BRADY JAMIE LOUISE (AU) ; COMMONW SCI INT IND

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ORIGIN
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  Best Local Similarity 98.5%; Pred. No. 1.9e-141;
  Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60
DB 110 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 169
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DB 170 ACAAGCAGAGGCTTGACCGCAATTCGATGAAGAACCTGTTAGGGTTAGCGTTTGGG 229
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DB 230 CTGCTCCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 289
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGGC 240
DB 290 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGGC 349
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QY 421 TTGGAGCAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTAGT 479
DB 530 TTGGAGCAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTAGT 589
QY 480 ACAATAAGCGCATTTGACCATTCACCATTTGGTGTGACCTC 523
DB 590 ACAATAAGCGCATTTGACCATTCACCATTTGGTGTGACCTC 633

RESULT 60
BD084805
LOCUS BD084805 11265 bp DNA linear PAT 27-AUG-2002
DEFINITION Enhancement of immune response using targeting molecules.
ACCESSION BD084805
VERSION BD084805.1 GI:22630415
KEYWORDS JP 2001522235-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 11265)
AUTHORS Boyle,J.S., Brady,J.L. and Lew,A.M.
TITLE Enhancement of immune response using targeting molecules
JOURNAL Patent: JP 2001522235-A 1 13-NOV-2001;
THE COUNCIL OF THE QUEENSLAND INSTITUTE OF MEDICAL RESEARCH, THE
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, THE
UNIVERSITY OF MELBOURNE, THE WALTER AND ELIZA HALL INSTITUTE OF
MEDICAL RESEARCH, CSL LTD
COMMENT OS Unidentified
PN JP 2001522235-A/1
PD 13-NOV-2001
PF 26-MAR-1998 AU PF 1998540989
PR 27-MAR-1997 AU PR 205891,13-FEB-1998 AU PP 1830 PI
JEFFEREY STEPHEN BOYLE, JAMIE LOUISE BRADY, ANDREW MARK LEW FC

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  Best Local Similarity 98.5%; Pred. No. 1.9e-141;
  Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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DB 230 CTGCTCCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 289
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DB 290 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGGC 349
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QY 421 TTGGAGCAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTAGT 479
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DB 590 ACAATAAGCGCATTTGACCATTCACCATTTGGTGTGACCTC 633

RESULT 61
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LOCUS AR202606 565 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 13 from patent US 6365151.
ACCESSION AR202606
VERSION AR202606.1 GI:21498779
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 565)
AUTHORS Halpern,M.S. and England,J.M.
TITLE Cellular immunogens comprising cognate proto-oncogenes
JOURNAL Patent: US 6365151-A 13 02-APR-2002;
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PUBMED  
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FEATURES  
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avian sarcoma virus and its cellular homolog  
Mol. Cell. Biol. 1 (11), 1024-1037 (1981)  
82271824

Location/Qualifiers

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ORIGIN

Query Match 90.2%; Score 472; DB 14; Length 565;  
Best Local Similarity 98.0%; Pred. No. 1.2e-132;  
Matches 490; Conservative 0; Mismatches 5; Indels 5; Gaps 1;  
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DB 1 GCTGAGTAGTCGCGAGCAAAATTAAGCTACACAGCAAGGCTTGACGACATTCG 60  
QY 88 ATGAAGAATCTGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGG 147  
DB 61 ATGAAGAATCTGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGG 120  
QY 148 TGCCTTACTCAGGAGCTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGG 207  
DB 121 ACAGGATCTCAGGAGCTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGG 180  
QY 208 GTTAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGAGGAGGAGGAGGAGT 267  
DB 181 GTTAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGAGGAGGAGGAGGAGT 240  
QY 268 CTTATGCAATCTCTTGTAGCTTTCACATG-----GTACGATGATGTAGCAATGCG 322  
DB 241 CTTATGCAATCTCTTGTAGCTTTCACATGCTTATGATGATGATGATGATGATGATG 300  
QY 323 CTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 382  
DB 301 CTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
QY 383 TGCCTTATTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 442  
DB 361 TGCCTTATTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

QY 443 CATTGCGAGATATTGATTAAAGTGCCTAGCTGATACATAAAGCCATTGACCAT 502  
DB 421 CATTGCGAGATATTGATTAAAGTGCCTAGCTGATACATAAAGCCATTGACCAT 480  
QY 503 CACCACATTGGTGCACCT 522  
DB 481 CACCACATTGGTGCACCT 500  
RESULT 64  
ALSRDCG 9317 bp RNA linear VRL 01-FEB-2000  
LOCUS Rous sarcoma virus genome, complete sequence.  
DEFINITION D10652  
ACCESSION D10652.1 GI:221012  
VERSION  
KEYWORDS core proteins; envelope protein; integrase; retroviral protease;  
reverse transcriptase; src oncogene, tyrosine kinase.  
SOURCE Rous sarcoma virus  
ORGANISM Rous sarcoma virus  
REFERENCE 1 (bases 1 to 9317)  
AUTHORS Kihira, Y.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 9317)  
AUTHORS Kihira, Y.  
TITLE Direct Submission  
JOURNAL Submitted (28-FEB-1992) Yasunori Kihira, Oriental Yeast Co., Ltd.,  
Nagahama Inst. for Biochemical Science; 50 Kano-cho, Nagahama,  
Shiga 526, Japan (Tel:0749-64-2346, Fax:0749-63-7910)  
Submitted (28-FEB-1992) to DDBJ by:  
Yasunori Kihira  
Nagahama Institute for Biochemical Science  
Oriental Yeast Co., Ltd.  
50 Kano-cho, Nagahama-shi  
Shiga 526  
Japan  
Phone: 0749-64-2346  
Fax: 0749-63-7910.  
FEATURES  
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## ORIGIN

Query Match 89.6%; Score 468.8; DB 12; Length 5647;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-131;  
 Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTAGTGCAGAGCAAAATTAAGCTTACA 60  
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 QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTCTTAG 180  
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 QY 241 TTTTGCATAGGGGGGGAATGTAGTCTTATGCAATCTCTTCTAGTCTTGCACATGG 300  
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 QY 301 TAACGATGATTAGCAACATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 360  
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 QY 361 TGGAGTAGGTGTACATCGTGCCTTATTAGGAGGCAACAGCGGGTCTGCATGGA 420  
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 QY 421 TTGGACCAACCACTAAATTCGCAATTCGAGAGATATTCTATTTAAGTGCTTA 472  
 Db TTGGACCAACCACTAAATTCGCAATTCGAGAGATATTCTATTTAAGTGCTTA 2577

## RESULT 66

XXU42372  
 LOCUS Cloning vector pOPRSVicat 6243 bp DNA circular SYN 07-MAR-2000  
 DEFINITION Cloning vector pOPRSVicat target vector from Lacswitch.  
 ACCESSION U42372  
 VERSION U42372.1 GI:1147761  
 KEYWORDS Cloning vector pOPRSVicat  
 SOURCE Cloning vector pOPRSVicat  
 ORGANISM Cloning vector pOPRSVicat  
 REFERENCE 1 (bases 1 to 6243)  
 AUTHORS Marsh, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-DEC-1995) Sam Marsh, Marketing, Stratagene, 11011  
 North Torrey Pines Road, La Jolla, CA 92037, USA  
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## ORIGIN

Query Match 89.6%; Score 468.8; DB 12; Length 6243;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-131;  
 Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTAGTGCAGAGCAAAATTAAGCTTACA 2165  
 QY 61 ACAGGCAAGGCTTACCGCAATTCGATGAAGATCTGTAGGTAGCGTTTGG 120  
 Db ACAGGCAAGGCTTACCGCAATTCGATGAAGATCTGTAGGTAGCGTTTGG 2225

QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGACTAGGTGTCTTAGG 180  
 Db CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGACTAGGTGTCTTAGG 2285  
 QY 181 CGAAAGCGGGCTTCGGTGTGTACGGGTTAGAGTCCCTCAGGATATAGTCTTGGC 240  
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## RESULT 67

AF052428  
 LOCUS Rous sarcoma virus strain Schmidt-Ruppin B, complete genome. 9396 bp DNA linear VRL 01-APR-1998  
 DEFINITION Rous sarcoma virus strain Schmidt-Ruppin B, complete genome.  
 ACCESSION AF052428  
 VERSION AF052428.1 GI:3003000  
 KEYWORDS Rous sarcoma virus  
 SOURCE Rous sarcoma virus  
 ORGANISM Rous sarcoma virus  
 REFERENCE 1 (bases 1 to 9396)  
 AUTHORS Bouck, J., Skalka, A.M. and Katz, R.A.  
 TITLE Complete nucleotide sequence of avian sarcoma virus  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 9396)  
 AUTHORS Bouck, J., Skalka, A.M. and Katz, R.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-MAR-1998) Fox Chase Cancer Center, 7701 Burholme Ave.,  
 Philadelphia, PA 19111, USA  
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Query Match 87.7%; Score 458.6; DB 14; Length 9396;  
Best Local Similarity 95.2%; Pred. No. 1.5e-128;  
Matches 500; Conservative 0; Mismatches 9; Indels 16; Gaps 2;

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Qy	121	CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGCTGCTTGG	180
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Qy	241	TTTTGCATAGGAGGGGGAATAGTCTTATGCAATACTCTTGTAGCTTTCGAACATG	299
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Db	9292	ACGGCTCTAACAGGATTGGACCAACCTAAATTCGCAATTCAGAGATTTGATTTA	9351
Qy	465	AGTGCCTAGCTCGATACATAAAGCCATTTGACCATTCACCACA	509
Db	9352	AGTGCCTAGCTCGATACATAAAGCCATTTGACCATTCACCACA	9396

RESULT 68  
REASVS  
LOCUS  
DEFINITION Avian sarcoma virus src gene and part of the env gene.  
ACCESSION V01169  
VERSION V01169.1 GI:61498  
KEYWORDS oncogene.



SOURCE Avian sarcoma virus  
ORGANISM Avian sarcoma virus  
REFERENCE 1 (bases 1 to 3107)  
AUTHORS Czerminofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M.,  
Tischer, E. and Goodman, H.M.  
TITLE Nucleotide sequence of an avian sarcoma virus oncogene (src) and  
proposed amino acid sequence for gene product  
JOURNAL Nature 287 (5779), 198-203 (1980)  
MEDLINE 81052295  
PUBMED 6253794  
REFERENCE 2 (bases 1 to 3107)  
AUTHORS Czerminofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M.,  
Tischer, E. and Goodman, H.  
TITLE Corrections to the nucleotide sequence of the src gene of Rous  
sarcoma virus  
JOURNAL Nature 301 (5902), 736-738 (1983)  
MEDLINE 83141780  
PUBMED 6298633  
REFERENCE 3 (bases 1 to 3107)  
AUTHORS Czerminofsky, A.P.  
TITLE Direct Submission  
JOURNAL Submitted (15-MAR-1983)  
COMMENT Contains corrections to the original sequence published in [1].  
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HDDTSDVQLQWGPATIFASILAPGVAQAQRIERLACWSKQANLTSILGLD  
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1123. .2703  
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/protein\_id="CAA24495.1"  
/db\_xref="GI:61499"  
/db\_xref="GOA:P00524"  
/db\_xref="SWISS-PROT:P00524"  
/translation="MSSSKPKDPSORRSLRPPDSTHHGGFPASQTPNKTAAPDTH  
RTPSPSGFTVATPKLPGFGNTSDTSPQAGALAGVTTFVALVDYSEWLETLSF  
KGERLQVWNTGKPNWLAHSITGTGTYGIPSNVAPSDSQAENWFKIETRESR  
LLINPENRGFTVRSSETTKGAYCLVSDFDNAGLVNKHVKIRKLDGSGYITST  
QFSSQLQVAYIKHADGLCHLNTVCPSTPQTKLADWEIPRESLRLVILGQG  
CFGEVWMTGNTGTRVAIKTLKPTGMSPEAFLOAQWKLRLHEKLVLYAVVSEPI  
YIVIEYMSKGLDLDLKGMGKYLRLPOLVMAAQTAGMAVVERMNVHRLRAANI  
LVGENLVCKVADGLRLJEDNEYTAGQAKFPIKWTAPEAALYGRFTIKSDVWSFGI  
LLETITKGRVPFGMGNEVLDVRVERGMPCCPCEPESLHDLMLCCQWRDPERPT  
FELYQLLPACVLEAVE"

Query Match 82.9%; Score 433.6; DB 14; Length 3107;  
Best Local Similarity 99.1%; Pred. No. 6.1e-121;  
Matches 436; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
2668 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 2727  
Db 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
Qy 61 ACAAGGCAAGGCTTACCGCAGCAATTCATGAAGATCTGCTTAGGCTTTAGCGTTTGGC 120

Db 2728 ACAAGGCAAGGCTTACCGCAGCAATTCATGAAGATCTGCTTAGGCTTAGCGTTTGGC 2787  
Qy 121 CTGCTTCCGATGTAGCGGCGAGATATTCGCTATCTAGGGGACTAGGGTGTGTAGG 180  
2788 CTGCTTCCGATGTAGCGGCGAGATATTCGCTATCTAGGGGACTAGGGTGTGTAGG 2847  
Qy 181 CGAAAAGCGGGGCTTCGGTGTAGCGGCTTAGGAGTCCCTTCAGGATATAGTAGTTGCG 240  
2848 CGAAAAGCGGGGCTTCGGTGTAGCGGCTTAGGAGTCCCTTCAGGATATAGTAGTTGCG 2907  
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTGTAGTCTTCAACATGG 300  
2908 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTGTAGTCTTCAACATGG 2967  
Qy 301 TAAAGATGTAGTACCAATGCTTACAGGAGAGAAAAGCAACCGCTGCATCGCATGG 360  
2968 TAAAGATGTAGTACCAATGCTTACAGGAGAGAAAAGCAACCGCTGCATCGCATGG 3027  
Qy 361 TGGAGTAAAGTGTACGATCGTCCCTTATTAGGAAGCAACAGCGGTCTGACATGGA 420  
3028 TGGAGTAAAGTGTACGATCGTCCCTTATTAGGAAGCAACAGCGGTCTGACATGGA 3087  
Qy 421 TTGACCAACCACTAAATTC 440  
Db 3088 TTGACCAACCACTAAATTC 3107  
RESULT 69  
XXU02432 8413 bp DNA circular SYN 29-JAN-1997  
DEFINITION Cloning vector pMAMneo, complete sequence.  
ACCESSION U02432  
VERSION U02432.1 GI:413798  
KEYWORDS Cloning vector pMAMneo  
SOURCE Cloning vector pMAMneo  
ORGANISM Cloning vector pMAMneo  
REFERENCE 1 (bases 1 to 8413)  
AUTHORS Kitts, P.A.  
TITLE ClONTECH Vectors On Disc version 1.3  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 8413)  
AUTHORS Kitts, P.A.  
TITLE Direct Submission  
JOURNAL Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,  
1020 East Meadow Circle, Palo Alto, CA 94303, USA  
COMMENT This vector can be obtained from CLONTECH Laboratories, Inc., 1020  
East Meadow Circle, Palo Alto, CA 94303, USA. To place an order  
call (415) 424-8222 or (800) 662-2566, extension 1. International  
customers, please contact your local distributor. For technical  
information, call (415) 424-8222 or (800) 662-2566, extension 3.  
This sequence has been compiled from information in the sequence  
databases, published literature and other sources, together with  
partial sequences obtained by CLONTECH; this vector has not been  
completely sequenced. If you suspect there is an error in this  
sequence, please contact CLONTECH's Technical Service Department at  
(415) 424-8222 or (800) 662-2566, extension 3 or E-mail  
TECH@CLONTECH.COM.  
FEATURES  
source  
1. .8413  
/organism="Cloning vector pMAMneo"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31818"

ORIGIN  
Query Match 82.4%; Score 430.8; DB 12; Length 8413;  
Best Local Similarity 99.5%; Pred. No. 4.4e-120;  
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
2780 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 8039  
Db 2780 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 8039

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QY      61  ACAAGCAAGGCTTGACCGACAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 120
Db      8040 ACAAGCAAGGCTTGACCGACAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 8099

QY      121 CTGCTTCGCATGTCAGGCGCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
Db      8100 CTGCTTCGCATGTCAGGCGCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 8159

QY      181 CGAAAAGCGGGGCTTCGGTTGTACGCGTTTAGGAGTCCCTCAGGATATAGTATTGCG 240
Db      8160 CGAAAAGCGGGGCTTCGGTTGTACGCGTTTAGGAGTCCCTCAGGATATAGTATTGCG 8219

QY      241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTCTTGTAGTCTTCAACATGG 300
Db      8220 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTCTTGTAGTCTTCAACATGG 8279

QY      301 TTAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAAGCACCGGTGATCCGATGG 360
Db      8280 TTAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAAGCACCGGTGATCCGATGG 8339

QY      361 TGGAGTAAAGTGTAGCAATGCTTATGCAATATCTCTTGTAGTCTTCAACATGGA 420
Db      8340 TGGAGTAAAGTGTAGCAATGCTTATGCAATATCTCTTGTAGTCTTCAACATGGA 8399

QY      421 TTGGACGAACCACT 434
Db      8400 TTGGACGAACCACT 8413

RESULT 70
XXU02430
LOCUS      XXU02430      8475 bp      DNA      circular SYN 29-JAN-1997
DEFINITION Cloning vector pMAMneoBlue, complete sequence.
ACCESSION  U02430
VERSION     U02430.1 GI:413796
KEYWORDS   Cloning vector pMAMneoBlue
SOURCE      Cloning vector pMAMneoBlue
ORGANISM    Cloning vector pMAMneoBlue
REFERENCE   1 (bases 1 to 8475);
AUTHORS     Kitts,P.A.
TITLE       Cloning Vectors On Disc version 1.3
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 8475)
AUTHORS     Kitts,P.A.
TITLE       Direct Submission
JOURNAL     Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
            1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT     This sequence has been compiled from information in the sequence
            databases, published literature and other sources, together with
            partial sequences obtained by CLONTECH. This vector is no longer
            available from CLONTECH and CLONTECH will not update or revise this
            sequence.

FEATURES             Location/Qualifiers
     source           1..8475
                     /organism="Cloning vector pMAMneoBlue"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:31821"

ORIGIN
Query Match      82.4%; Score 430.8; DB 12; Length 8475;
Best Local Similarity 99.5%; Pred. No. 4.4e-120;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTGAGTGTGCTGAGTGTGCGGAGCAAAATTTAGCTACA 60
Db      8042 CTGCTCCCTGCTGTGTGTGAGTGTGCTGAGTGTGCGGAGCAAAATTTAGCTACA 8101

QY      61  ACAAGCAAGGCTTGACCGACAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 120
Db      8102 ACAAGCAAGGCTTGACCGACAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 8161

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QY      121 CTGCTTCGCATGTCAGGCGCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
Db      8162 CTGCTTCGCATGTCAGGCGCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 8221

QY      181 CGAAAAGCGGGGCTTCGGTTGTACGCGTTTAGGAGTCCCTCAGGATATAGTATTGCG 240
Db      8222 CGAAAAGCGGGGCTTCGGTTGTACGCGTTTAGGAGTCCCTCAGGATATAGTATTGCG 8281

QY      241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTCTTGTAGTCTTCAACATGG 300
Db      8282 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTCTTGTAGTCTTCAACATGG 8341

QY      301 TTAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAAGCACCGGTGATCCGATGG 360
Db      8342 TTAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAAGCACCGGTGATCCGATGG 8401

QY      361 TGGAGTAAAGTGTAGCAATGCTTATGCAATATCTCTTGTAGTCTTCAACATGGA 420
Db      8402 TGGAGTAAAGTGTAGCAATGCTTATGCAATATCTCTTGTAGTCTTCAACATGGA 8461

QY      421 TTGGACGAACCACT 434
Db      8462 TTGGACGAACCACT 8475

RESULT 71
XXU02431
LOCUS      XXU02431      9184 bp      DNA      circular SYN 29-JAN-1997
DEFINITION Cloning vector pMAMneo-CAT, complete sequence.
ACCESSION  U02431
VERSION     U02431.1 GI:413797
KEYWORDS   Cloning vector pMAMneo-CAT
SOURCE      Cloning vector pMAMneo-CAT
ORGANISM    Cloning vector pMAMneo-CAT
REFERENCE   1 (bases 1 to 9184);
AUTHORS     Kitts,P.A.
TITLE       Cloning Vectors On Disc version 1.3
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 9184)
AUTHORS     Kitts,P.A.
TITLE       Direct Submission
JOURNAL     Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
            1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT     This vector can be obtained from CLONTECH Laboratories, Inc., 1020
            East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
            call (415) 424-8222 or (800) 662-2566, extension 1. International
            customers, please contact your local distributor. For technical
            information, call (415) 424- 8222 or (800) 662-2566, extension 3.
            This sequence has been compiled from information in the sequence
            databases, published literature and other sources, together with
            partial sequences obtained by CLONTECH; this vector has not been
            completely sequenced. If you suspect there is an error in this
            sequence, please contact CLONTECH's Technical Service Department at
            (415) 424-8222 or (800) 662-2566, extension 3 or E-mail
            TECH@CLONTECH.COM.

FEATURES             Location/Qualifiers
     source           1..9184
                     /organism="Cloning vector pMAMneo-CAT"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:31819"

ORIGIN
Query Match      82.4%; Score 430.8; DB 12; Length 9184;
Best Local Similarity 99.5%; Pred. No. 4.4e-120;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTGAGTGTGCTGAGTGTGCGGAGCAAAATTTAGCTACA 60
Db      8751 CTGCTCCCTGCTGTGTGTGAGTGTGCTGAGTGTGCGGAGCAAAATTTAGCTACA 8810

QY      61  ACAAGCAAGGCTTGACCGACAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 120

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Db      8811  ACAAGGCAAGGCTTGACCGACAAATTGCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 8870
QY      121  CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGCGGACTAGGGTGTGTTAGG 180
Db      8871  CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGCGGACTAGGGTGTGTTAGG 8930
QY      181  CGAAAAAGGGGGCTTCGGTTGTACGCGGTAGAGGATCCCTCAGGATATAGTAGTTTCG 240
Db      8931  CGAAAAAGGGGGCTTCGGTTGTACGCGGTAGAGGATCCCTCAGGATATAGTAGTTTCG 8990
QY      241  TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db      8991  TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 9050
QY      301  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360
Db      9051  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 9110
QY      361  TGAAGTAAAGTGGTACGATCGTGTCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 420
Db      9111  TGAAGTAAAGTGGTACGATCGTGTCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 9170
QY      421  TTGGACGAAACCACT 434
Db      9171  TTGGACGAAACCACT 9184

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RESULT 72
LOCUS    U02448                      10339 bp    DNA    circular SYN 29-MAR-1995
DEFINITION Cloning vector pMAMneo-LUC, complete sequence.
ACCESSION U02448
VERSION    U02448.1 GI:413814
KEYWORDS
SOURCE     Cloning vector pMAMneo-LUC
ORGANISM   Cloning vector pMAMneo-LUC
REFERENCE  1 (bases 1 to 10339)
            Kitts, P.A.
            CLONTECH Vectors On Disc version 1.3
            Unpublished
            Kitts, P.A.
REFERENCE  2 (bases 1 to 10339)
            Direct Submission
            Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
            1020 East Meadow Circle, Palo Alto, CA 94303, USA
            In reference 2, this vector is referred to as pBSpac delta P. This
            vector can be obtained from CLONTECH Laboratories, Inc., 1020 East
            Meadow Circle, Palo Alto, CA 94303, USA. To place an order call
            (415) 424-8222 or (800) 662-2566, extension 1. International
            customers, please contact your local distributor. For technical
            information, call (415) 424- 8222 or (800) 662-2566, extension 3.
            This sequence was compiled by Susana de la Luna. If you suspect
            there is an error in this sequence, please contact CLONTECH's
            Technical Service Department at (415) 424-8222 or (800) 662-2566,
            extension 3 or E-mail TECH@CLONTECH.COM.

```

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FEATURES
Source
1..10339
    /organism="Cloning vector pMAMneo-LUC"
    /mol_type="genomic DNA"
    /db_xref="taxon:31820"

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ORIGIN
Query Match      82.4%; Score 430.8; DB 12; Length 10339;
Best Local Similarity 99.5%; Pred. No. 4.4e-120;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1  CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db      9906  CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 9965
QY      61  ACAAGGCAAGGCTTGACCGACAAATTGCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 120

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Db      9966  ACAAGGCAAGGCTTGACCGACAAATTGCATGAAGATCTGCTTAGGGTTAGGCGTTTTCG 10025
QY      121  CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGCGGACTAGGGTGTGTTAGG 180
Db      10026  CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGCGGACTAGGGTGTGTTAGG 10085
QY      181  CGAAAAAGGGGGCTTCGGTTGTACGCGGTAGAGGATCCCTCAGGATATAGTAGTTTCG 240
Db      10086  CGAAAAAGGGGGCTTCGGTTGTACGCGGTAGAGGATCCCTCAGGATATAGTAGTTTCG 10145
QY      241  TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db      10146  TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 10205
QY      301  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360
Db      10206  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 10265
QY      361  TGAAGTAAAGTGGTACGATCGTGTCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 420
Db      10266  TGAAGTAAAGTGGTACGATCGTGTCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 10325
QY      421  TTGGACGAAACCACT 434
Db      10326  TTGGACGAAACCACT 10339

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RESULT 73
LOCUS    BD268238                      11600 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION Adenovirus vector, packaging cell line, composition and method for
            production and use.
ACCESSION BD268238
VERSION    BD268238.1 GI:33078006
KEYWORDS   JP 2002534130-A/42.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 11600)
            Nemerow, G.R., Seggern, D.J.V., Hallenbeck, P.L., Stevenson, S.C. and
            Skripchenko, Y.
            Adenovirus vector, packaging cell line, composition and method for
            production and use
            Patent: JP 2002534130-A 42 15-OCT-2002;
            NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
            OS Artificial Sequence
            PN JP 2002534130-A/42
            PD 15-OCT-2002
            PP 14-JAN-2000 JP 2000593765
            PR 14-JAN-1999 US 60/115920
            PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI
            SUSAN C STEVENSON, YELENA SKRIPCHENKO
            PC C12N15/09, A61K35/76, A61K46/00, A61P35/00, A61P43/00, A61P43/00,
            PC C12N5/10,
            PC C12N7/00, C12Q1/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
            Description of Artificial Sequence: plasmid
            FH Key Location/Qualifiers
            FT source 1..11600
            /organism='Artificial Sequence'.

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source
1..11600
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

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ORIGIN
Query Match      82.4%; Score 430.8; DB 6; Length 11600;
Best Local Similarity 99.5%; Pred. No. 4.5e-120;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1  CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db      11167  CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 11226

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QY 61 ACAGCGAAGGCTTGACCGCAATTCGATGAGAACTCTCTAGGGTTAGCGGTTTTCGC 120
Db 11227 ACAAGCGAAGGCTTGACCGCAATTCGATGAGAACTCTCTAGGGTTAGCGGTTTTCGC 11286
QY 121 CTCGCTTCGCGATGTACCGGCCAGATATTTCGCGTATCTCTAGGGGCACTAGGGGTGTGTTTAG 180
Db 11287 CTCGCTTCGCGATGTACCGGCCAGATATTTCGCGTATCTCTAGGGGCACTAGGGGTGTGTTTAG 11346
QY 181 CGAAAAGCGGGCTTCGCGTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240
Db 11347 CGAAAAGCGGGCTTCGCGTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 11406
QY 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTCTAGTCTTGCACATGC 300
Db 11407 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTCTAGTCTTGCACATGC 11466
QY 301 TAAAGTATGTTAGCACATCGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
Db 11467 TAAAGTATGTTAGCACATCGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 11526
QY 361 TGAAGTAAAGTGTGATCGTGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420
Db 11527 TGAAGTAAAGTGTGATCGTGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 11586
QY 421 TTGGACGACCACT 434
Db 11587 TTGGACGACCACT 11600

RESULT 74
RSU41727 874 bp DNA linear VRL 18-JUL-2001
LOCUS Rous sarcoma virus Schmidt-Ruppin subgroup A (NY) clone iPH2013-4,
DEFINITION Sp37 (env) gene, partial cds, and 3'/LTR.
ACCESSION U41727
VERSION U41727.1 GI:1136589
KEYWORDS Rous sarcoma virus
SOURCE Rous sarcoma virus
ORGANISM Rous sarcoma virus
REFERENCE 1 (bases 1 to 532)
AUTHORS Hara.H. and Kaji.A.
TITLE The U3 region of the long terminal repeat of a subgroup A
transformation-defective rous sarcoma virus (tdPH2010) converts a
necropathic virus to a cytopathic virus
JOURNAL Virus Genes 15 (2), 171-180 (1997)
MEDLINE 98083689
PUBMED 9421881
REFERENCE 2 (bases 1 to 874)
AUTHORS Hara.H.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1995) Hiroto Hara, University of Pennsylvania
School of Medicine, Microbiology, 573 Maloney Building, 36th and
Spruce Street, Philadelphia, PA 19104-4283, USA
FEATURES
source
1. 874
/organism="Rous sarcoma virus"
/proviral
/moi_type="genomic DNA"
/strain="Schmidt-Ruppin subgroup A (NY)"
/specific_host="Gallus gallus"
/db_xref="taxon:11886"
/clone="lambda iPH2013-4"
/lab_host="Gallus gallus"
1. .35
/gene="env"
<1. .35
/gene="env"
/function="envelope transmembrane protein"
/codon_start=3
/product="gp37"
/protein_id="AAB60581.1"

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/db_xref="GI:1136590"
/translation="AYQPESEIV"
76. .191
/note="direct; drl (left)"
372. .373
/organism="Rous sarcoma virus"
414. .533
/note="src deletion site"
/note="direct; drl (right)"
542. .874
/note="3' LTR"
542. .775
/note="U3"
misc_difference 650
/note="T in transformation-defective, cytopathic strain
tdPH2010"
/misc_difference 753
/note="A in transformation, cytopathic strain tdPH2010"
/replacement="a"
776. .796
/note="R"
797. .874
/note="U5"
ORIGIN
Query Match 78.4%; Score 409.8; DB 14; Length 874;
Best Local Similarity 97.3%; Pred. No. 1.1e-113;
Matches 429; Conservative 0; Mismatches 7; Indels 5; Gaps 1;
QY 87 CATGAGAAATCTCTAGGGTTAGGCGTTTTCGCTCTTCGCGATGTAAGGCGGCAATA 146
Db 369 CGTAAAGAAATCTCTAGGGTTAGGCGTTTTCGCTCTTCGCGATGTAAGGCGGCAATA 428
QY 147 TTCGCGATCTGAGGGGCTAGGGTCTGTTAGGCGGAAAGCGGGCTTCGTTGTAAGC 206
Db 429 TACGTGTATCTGAGGGGCTAGGGTCTGTTAGGCGGAAAGCGGGCTTCGTTGTAAGC 488
QY 207 GGTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGCGGAAATAG 266
Db 489 GTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGCGGAAATAG 548
QY 267 TCTTATGCAATCTCTAGTCTTGCACATG-----GTAACGATGAGTTAGCAATG 321
Db 549 TCTTATGCAATCTCTAGTCTTGCACATGCTTATGTAACGATGAGTTAGCAATG 608
QY 322 CTTTACAGGAGGAGAAAGCAACCGTGCATGCGGATGTTGGAAGTAAGGTGTACGATC 381
Db 609 CTTTACAGGAGGAGAAAGCAACCGTGCATGCGGATGTTGGAAGTAAGGTGTACGATC 668
QY 382 GTGCTTTATTAGGAGGCAACAGACGCGGTCTGCATGAGTTGGACGAACTAAATTC 441
Db 669 GTGCTTTATTAGGAGGCAACAGACGCGGTCTGCATGAGTTGGACGAACTAAATTC 728
QY 442 GCATTGAGAGATATTGATTTAGTCCCTAGCTCGATACATTAACGCGCATTTGACAT 501
Db 729 GCATTGAGAGATATTGATTTAGTCCCTAGCTCGATACATTAACGCGCATTTGACAT 788
QY 502 TCACCAATTTGGTGTGCACCT 522
Db 789 TCACCAATTTGGTGTGCACCT 809

RESULT 75
BD268239 8238 bp DNA linear PAT 17-JUL-2003
LOCUS Adenovirus vector, packaging cell line, composition and method for
DEFINITION production and use.
ACCESSION BD268239
VERSION BD268239.1 GI:33078007
KEYWORDS JP 2002534130-A/43.
SOURCE synthetic construct
ORGANISM synthetic construct

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artificial sequences.
1 (bases 1 to 8238)
REFERENCE Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and
AUTHORS Skripchenko,Y.
TITLE Adenovirus vector, packaging cell line, composition and method for
JOURNAL production and use
COMMENT Patent: JP 2002534130-A 43 15-OCT-2002;
NOVARTIS AG,THE SCRIPPS RESEARCH INSTITUTE
CS Artificial Sequence
PN JP 2002534130-A/43
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593765
PR 14-JAN-1999 US 60/115920
PI GLEN ROBERT NEMEROW,DANIEL J VON SEGGERN,PAUL L HALLENBECK, PI
SUSAN C STEVENSON,YELENA SKRIPCHENKO
PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00,
PC C12N5/10,C12N1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
PC C12N7/00,C12N1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
Description of Artificial Sequence: plasmid
FH Key Location/Qualifiers
FT source 1..8238
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..8238
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 75.1%; Score 393; DB 6; Length 8238;
Best Local Similarity 98.8%; Pred.No.1.5e-108;
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 123 GCTTCCGAGTGTACGGCGACGATATTCGCTATCTGAGGGGACTAGGGTGTGTTTAGGG 182
Db 404 GCGCCCGGATGTACGGCGCGAGATACCGGTATCTGAGGGGACTAGGGTGTGTTTAGGG 463
QY 183 AAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242
Db 464 AAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 523
QY 243 TTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTGTAGTCTTGCAACATGGTA 302
Db 524 TTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTGTAGTCTTGCAACATGGTA 583
QY 303 ACATGAGTTAGCAACATGCTTACAGGAGAGAAAGCACCGTCATGCCGATTGGTG 362
Db 584 ACATGAGTTAGCAACATGCTTACAGGAGAGAAAGCACCGTCATGCCGATTGGTG 643
QY 363 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAACAGACGGGTCTGACATGGATT 422
Db 644 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAACAGACGGGTCTGACATGGATT 703
QY 423 GGACGACCACTAAATTCGCGATTCGAGGATATGTATTAGTGCCTAGCTCGATACA 482
Db 704 GGACGACCACTAAATTCGCGATTCGAGGATATGTATTAGTGCCTAGCTCGATACA 763
QY 483 ATAAAGCCATTTCACCATTCACCATTCACCATTCACCATTCACCATTCACCATTC 523
Db 764 ATAAAGCCATTTCACCATTCACCATTCACCATTCACCATTCACCATTCACCATTC 804

```

Search completed: March 11, 2004, 09:42:27  
Job time : 2938.11 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 03:02:06 ; Search time 451.626 Seconds  
(without alignments)  
4919.575 Million cell updates/sec

Title: US-09-733-368a-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgtctccgttggtgtgtt.....accacattgtgtgcacctc 523

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N Geneseq\_29Jan04.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002s.\*

7: geneseqn2003as.\*

8: geneseqn2003bs.\*

9: geneseqn2003cs.\*

10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523	100.0	648	4	Aah43951 Rous sarc
2	519.8	99.4	7086	9	Adh35600 Tricistron
3	517.8	99.0	2245	7	Abz23249 Lac repre
4	515	98.5	4965	2	Aag75973 pHLA-B*7/b
5	513.8	98.2	562	7	Abz23250 Nucleotid
6	508.8	97.3	4457	9	Adh35599 Bicistron
7	508.8	97.3	7334	9	Adh35601 Tetraclst
8	505.6	96.7	4059	2	Aag75974 pHLA-B*7 e
9	505.6	96.7	4341	6	Aag62391 Vector pv
10	505.6	96.7	4341	6	Asl17704 Vector pv
11	505.6	96.7	4341	6	Adh35143 Plasmid p
12	505.6	96.7	5653	2	Aat02998 RSV tar R
13	505.6	96.7	5653	2	Aat76802 RSV tar R
14	505.6	96.7	5750	2	AaQ43814 pRLD3D4 C
15	505.6	96.7	6207	2	AaQ43813 pRLD2D3D4
16	505.6	96.7	6274	2	AaQ43812 pRLD1D2D3
17	505.6	96.7	8591	2	Aat84562 Plasmid p
18	505.6	96.7	8591	2	Aat84561 Plasmid p
19	505.6	96.7	8591	2	Aat87083 Plasmid p
20	505.6	96.7	8591	2	Aat87084 Plasmid p
21	505.6	96.7	8591	2	Aav04866 cDNA enco
22	505.6	96.7	8591	2	Aav04865 cDNA enco
23	505.6	96.7	8591	2	Aav05850 APP-REP 7

Aav05849 APP-REP 7  
Aat62602 Luciferas  
Aaa53869 Expressio  
Abl57333 Vector pl  
Aaa53873 Expressio  
Aaa53879 Expressio  
Aaa53875 Expressio  
Aaa53874 Expressio  
Aaa53876 Expressio  
Aat71261 Rous sarc  
Aaz60824 Nucleotid  
Aaa59077 Nucleotid  
Aba94279 Nucleotid  
Aaa56865 DNA seque  
Adb75125 Chromosom  
Aaa14722 Nucleotid  
Aaz93333 Partial s  
Aaz93078 Partial s  
Aaz93331 Partial s  
Aaz93079 Partial s  
Aac89169 AdRSVpHYD  
Aaa09085 AdRSV-bet  
Aaa59078 Nucleotid  
Aaa56867 DNA seque  
Aaz94163 Adenoviru  
Aaa56866 DNA seque  
Aaz29699 Viral exp  
Aaa55269 DNA of ex  
Aaz94161 395 Nucle  
Aaa14719 Nucleotid  
Aaz93077 Rous Sarc  
Aaz02780 Vector pM  
Aax02997 Bovine sc  
Aad28272 LSRNL vec  
Aad28311 LSRNL vec  
Aaa5665 Human res  
Aaa06310 Sequence  
Aaa06311 Sequence  
Aaa06309 Sequence  
Aaa06313 Sequence  
Aaa06312 Sequence  
Aad27899 pmt2 vec  
Aac92489 Fragment  
Aax77359 Polynucle  
Aaa90391 987Bbreo  
Aaz27850 Complete  
Aad04741 Alphavira  
Aaf84024 Complete  
Aab10062 Expressio  
Aad53272 MSV2/EGF  
Aad53270 MSV2/ACT  
Aad53271 MSV2/IRE  
Aad14296 MSV2/EGF  
Aad13899 Recombina  
Aad53274 MSV2/EGF  
Aad53290 MSV2/EGF  
Aad53293 MSV2/EGF  
Aad53292 MSV2/EGF  
Aad53273 MSV2/EGF  
Aad53289 MSV2/EGF  
Aad53291 MSV2/EGF  
Aad14199 MSV2/EGF  
Aad14203 MSV2/EGF  
Abl90071 Human pol  
Aav58058 Plasmid C  
Aad02037 Plasmid p  
Aad02036 Plasmid p  
Aat62937 3f4 human  
Aat62932 2a2 human  
Aav40006 Plasmid p  
Aat90695 Plasmid C  
Aav40007 Plasmid p

97 151.4 28.9 4249 2 AAV63466 Plasmid p  
98 151.4 28.9 4597 4 AAF24901 Nucleotide  
99 151.4 28.9 4840 4 AAF83146 Complete  
100 151.4 28.9 5015 9 ADB33528 Expressio

ALIGNMENTS

RESULT 1  
AAH43951  
ID AAH43951 standard; DNA; 648 BP.  
XX  
AC AAH43951;  
XX  
DT 06-SEP-2001 (first entry)  
XX  
DE Rous sarcoma virus promoter nucleotide sequence SEQ ID NO:1.  
XX  
KW Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression;  
KW transgene; genetic engineering; gene therapy; immunisation; ds.  
XX  
OS Rous sarcoma virus.  
XX  
PN WO200142444-A2.  
XX  
PD 14-JUN-2001.  
XX  
PF 08-DEC-2000; 2000WO-US033256.  
XX  
PR 10-DEC-1999; 99US-0170019P.  
XX  
PA (ARIA-) ARIAD GENE THERAPEUTICS INC.  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Rivera V, Zolnick P, Wilson JM;  
XX WPI; 2001-381673/40.  
XX  
PT Genetically engineering a primate for expression of a desired gene,  
PT comprises introducing into the primate a transgene comprising Rous  
PT Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to  
PT RSV promoter.  
XX  
PS Claim 7; Page 44; 64pp; English.  
XX  
CC The present invention describes a method for genetically engineering a  
CC primate for expression of a desired gene comprising introducing into the  
CC primate a transgene comprising an Rous Sarcoma Virus (RSV) promoter and a  
CC nucleic acid sequence heterologous to RSV promoter. Also described is a  
CC primate cell (i) containing and capable of expressing a transgene  
CC comprising an RSV promoter operably linked to a recombinant nucleic acid  
CC encoding one or more fusion proteins, where the fusion proteins bind to a  
CC ligand and in the presence of the ligand modulate(s) the expression level  
CC of a target gene. The method can be used for high level expression of  
CC genes in primates or for engineering primate cells. It is useful for  
CC increasing the efficacy of many gene therapy strategies, and for  
CC like ribozymes, antisense RNA, and dominant negative proteins, that act  
CC either stoichiometrically, or by competition. The method increases the  
CC efficacy of many gene therapy strategies by substantially elevating the  
CC expression of an exogenous therapeutic gene, and allowing expression to  
CC reach therapeutically effective levels. The present sequence represents a  
CC specifically claimed RSV enhancer/promoter nucleotide sequence from the  
CC present invention  
XX  
SQ Sequence 648 BP; 163 A; 135 C; 179 G; 171 T; 0 U; 0 Other;

Query March 100.0%; Score 523; DB 4; Length 648;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGGAGGTCGTAGTAGTCGGCGGACCAAAATTTAGCTACA 60

Db 90 CTGCTCCCTGCTGTGTGTGGAGGTCGTAGTAGTCGGCGGACCAAAATTTAGCTACA 149  
QY 61 ACAGGCGAGGCTTCAGCGCAATTCATGAGGAATCTGCTTAGGGTTAGCGTTTGGCG 120  
Db 150 ACAAGGCGAGGCTTCAGCGCAATTCATGAGGAATCTGCTTAGGGTTAGCGTTTGGCG 209  
QY 121 CTGCTTCGGGATGTACGGGGCCAGATATTCGGGTATCTAGGGGACTAGGGTGTCTTTAGG 180  
Db 210 CTGCTTCGGGATGTACGGGGCCAGATATTCGGGTATCTAGGGGACTAGGGTGTCTTTAGG 269  
QY 181 CGAAAAGCGGGCTTCGGGTTGTACGGGTTAGGAGTCCCTCAGAGATATAGTAGTTTCGC 240  
Db 270 CGAAAAGCGGGCTTCGGGTTGTACGGGTTAGGAGTCCCTCAGAGATATAGTAGTTTCGC 329  
QY 241 TTTTGCATATAGGGGAGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGG 300  
Db 330 TTTTGCATATAGGGGAGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGG 389  
QY 301 TAACGATGATTTAGCAACATGCCCTTACAAAGGAGAGAAAAGCAACCGTGATGCCGATGG 360  
Db 390 TAAAGATGATTTAGCAACATGCCCTTACAAAGGAGAGAAAAGCAACCGTGATGCCGATGG 449  
QY 361 TGGAGTATAGGTTGATACGATCGCTTATTTAGGAGGCAACAGCGGCTCTGCACATGGA 420  
Db 450 TGGAGTATAGGTTGATACGATCGCTTATTTAGGAGGCAACAGCGGCTCTGCACATGGA 509  
QY 421 TTGGACGAACCACTAAATTCGGCATTTGCAGAGATATTTAGTGTCTAGCTCGATA 480  
Db 510 TTGGACGAACCACTAAATTCGGCATTTGCAGAGATATTTAGTGTCTAGCTCGATA 569  
QY 481 CAATPAAAGCCATTTGACCATTCACCATTCACCATTCACCATTCACCATTC 523  
Db 570 CAATPAAAGCCATTTGACCATTCACCATTCACCATTCACCATTCACCATTC 612

RESULT 2  
ADD35600/c  
ID ADD35600 standard; DNA; 7086 BP.  
XX  
AC ADD35600;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Tricistronic eukaryotic expression vector PL249.  
XX  
KW Multicistronic eukaryotic expression vector; multiple protein expression;  
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;  
KW chain terminator; transcription pause site; gene transfer;  
KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;  
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;  
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;  
KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;  
KW MRGB terminator; cyclic; circular; ds.  
OS Chimeric.  
OS Synthetic.  
OS Human herpesvirus 5.  
OS Encephalomyocarditis virus.  
OS Simian virus 40.  
OS Rous sarcoma virus.  
OS Cryptolagus cuniculus.  
OS Escherichia coli.  
XX  
PN WO2003031630-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 10-OCT-2002; 2002WO-IT000646.  
XX  
PR 12-OCT-2001; 2001IT-MI002110.  
XX  
PA (KERY-) KERYOS SPA.

XX Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;  
 XX WPI; 2003-393446/37.  
 XX New multicistronic recombinant plasmid vectors expressing two to our  
 XX genes simultaneously, useful in various biotechnological applications,  
 XX such as gene transfer, gene therapy and in DNA immunization.  
 XX Claim 18; SEQ ID NO 3; 52pp; English.  
 XX The invention relates to multicistronic eukaryotic expression vectors for  
 XX the expression of at least two proteins of interest which may be  
 XX identical or different. The vectors comprise at least one eukaryotic  
 XX expression cassette having a promoter/enhancer sequence, an intron  
 XX sequence, a cloning site, a viral internal ribosomal entry site (IRES)  
 XX and a chain terminator. The vectors may additionally contain a  
 XX transcription pause site downstream of the chain terminator. The  
 XX invention also encompasses eukaryotic host cells comprising a vector of  
 XX the invention, and the recombinant expression of two or more eukaryotic  
 XX proteins using host cells transformed with a vector of the invention.  
 XX The vectors are useful in various biotechnological applications in which  
 XX the simultaneous expression of two or more genes is necessary, such as  
 XX gene transfer protocols, DNA immunisation, or for the expression of  
 XX different molecules in the same cell. They may also be used in gene  
 XX therapy. The present sequence represents a specifically claimed vector  
 XX designated PL249, which comprises a cytomegalovirus (CMV)  
 XX promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)  
 XX IRES, an SV40 polyadenylation site, a transcription pause site, a Rous  
 XX sarcoma virus (RSV) promoter, rabbit beta-globin intron, and a rabbit  
 XX beta-globin gene mRGE terminator as well as a kanamycin resistance gene.  
 XX Sequence 7086 BP; 1870 A; 1699 C; 1753 G; 1764 T; 0 U; 0 Other;  
 XX  
 Query Match 99.4%; Score 519.8; DB 9; Length 7086;  
 Best Local Similarity 99.6%; Pred. No. 8.3e-172;  
 Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
 Db 2055 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1996  
 QY 61 ACAAGGCAAGGCTTACCGCAATTCATGAAGAATCTCTTGGGTTAGCGTTTGGC 120  
 Db 1995 ACAAGGCAAGGCTTACCGCAATTCATGAAGAATCTCTTGGGTTAGCGTTTGGC 1936  
 QY 121 CTGCTCCGAGTACCGGCGAGATTCGCGTATCTGAGGAGTACGGTGTGTAGG 180  
 Db 1935 CTGCTCCGAGTACCGGCGAGATTCGCGTATCTGAGGAGTACGGTGTGTAGG 1876  
 QY 181 CGAAAGCGGGCTTCGGTTGTACGCGTTAGGAGTCCCTCAGGATATAGTATTCGC 240  
 Db 1875 CGAAAGCGGGCTTCGGTTGTACGCGTTAGGAGTCCCTCAGGATATAGTATTCGC 1816  
 QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGAACATGG 300  
 Db 1815 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGAACATGG 1756  
 QY 301 TACGATGAGTACCAATCTTACAGGAGGAGAAAGCAACCGTGCATCCGATTTGG 360  
 Db 1755 TACGATGAGTACCAATCTTACAGGAGGAGAAAGCAACCGTGCATCCGATTTGG 1696  
 QY 361 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACCGGTTGACATGGA 420  
 Db 1695 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACCGGTTGACATGGA 1636  
 QY 421 TTGAGCGAACCACTAATCTCGGATTCGAGAGATTTGTATTAAAGTCCCTAGCTGATA 480  
 Db 1635 TTGAGCGAACCACTAATCTCGGATTCGAGAGATTTGTATTAAAGTCCCTAGCTGATA 1576  
 QY 481 CAAATACCGCAATTTGACCAATTCACCAATTTGCTGACCTC 523  
 Db 1575 CAAATACCGCAATTTGACCAATTCACCAATTTGCTGACCTC 1533

RESULT 3  
 ABZ23249  
 ID ABZ23249 standard; DNA; 2245 BP.  
 XX  
 XX ABZ23249;  
 XX  
 XX 24-VAR-2003 (first entry)  
 XX  
 XX Lac repressor operated p21-expression cassette and RSV-LTR promoter.  
 XX  
 XX Lac repressor; p21; RSV; LTR promoter; cell cycle inhibitor protein;  
 XX protein production; anchorage-independent producer cell line; ss.  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX Promoter i. .563  
 XX /tag= a  
 XX /note= "RSV-LTR promoter"  
 XX Intron 564. .1051  
 XX /tag= b  
 XX /note= "SV40 small t antigen intron"  
 XX misc\_feature 1052. .1907  
 XX /tag= c  
 XX /note= "p21 coding sequence"  
 XX polyA\_signal 1908. .2245  
 XX /tag= d  
 XX /note= "thymidine kinase polyA site"  
 XX  
 XX WO200299100-A2.  
 XX  
 XX 12-DEC-2002.  
 XX  
 XX 03-JUN-2002; 2002WO-BP006054.  
 XX  
 XX 01-JUN-2001; 2001GB-00013318.  
 XX  
 XX (LONZ ) LONZA BIOLOGICS PLC.  
 XX  
 XX Al-Rubeai M, Shuttleworth J;  
 XX  
 XX WPI; 2003-148669/14.  
 XX  
 XX Producing recombinant protein, particularly for maximizing or enhancing  
 XX e.g. therapeutic protein production, by co-expressing protein with  
 XX recombinant cell cycle inhibitor protein (p21) in producer cell line.  
 XX  
 XX Example 1; Page 15-16; 33pp; English.  
 XX  
 XX The present sequence represents a lac repressor operated p21-expression  
 XX cassette comprising the Rous sarcoma virus (RSV)-LTR promoter. p21 is a  
 XX cell cycle inhibitor protein. The present sequence is used to produce  
 XX vectors for use in the method of the invention. The specification  
 XX describes a method for producing a protein, preferably a recombinant  
 XX protein, in a mammalian anchorage-independent producer cell line. The  
 XX method comprises co-expressing with the protein in the producer cell line  
 XX a recombinant cell cycle inhibitor protein (preferably p21). The method  
 XX is useful for producing a recombinant protein in a producer cell line.  
 XX This is particularly useful for maximizing or enhancing the production of  
 XX e.g. therapeutic proteins at an industrial scale  
 XX  
 XX Sequence 2245 BP; 532 A; 555 C; 625 G; 533 T; 0 U; 0 Other;  
 XX  
 Query Match 99.0%; Score 517.8; DB 7; Length 2245;  
 Best Local Similarity 99.6%; Pred. No. 2.3e-171;  
 Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
 Db 46 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 105



```

QY 61 ACAAGGCAAGCTTGCACCAATTCATGAAGAACTCTCTTAGGGTTAGGCGCTTTTCGC 120
Db 106 ACAAGGCAAGCTTGCACCAATTCATGAAGAACTCTCTTAGGGTTAGGCGCTTTTCGC 165
QY 121 CTGCTTCGCGATGACGGGCGCAGATATTCGCGTATCTGAGGGAAGCTAGGCTGCTTAGG 180
Db 166 CTGCTTCGCGATGACGGGCGCAGATATTCGCGTATCTGAGGGAAGCTAGGCTGCTTAGG 225
QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGATATAGTATGTTTCGC 240
Db 226 CGAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGATATAGTATGTTTCGC 285
QY 241 TTTTTCATAGGAGGAGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
Db 286 TTTTTCATAGGAGGAGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGG 345
QY 301 TAACGATGATGACACATGCTTACAGGAGAGAGAAAGACCGTGCTATCGGATGG 360
Db 346 TAACGATGATGACACATGCTTACAGGAGAGAGAAAGACCGTGCTATCGGATGG 405
QY 361 TGGAGTAAAGTGTAGTACGATCGTGTCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420
Db 406 TGGAGTAAAGTGTAGTACGATCGTGTCTTATTAGGAGGCAACAGACGGGTCTGACATGA 465
QY 421 TTGGACGAAACCAATTAATTCGCAATTCAGAGATATTTATTTAAGTGCCTAGCTCGATA 480
Db 466 TTGGACGAAACCAATTAATTCGCAATTCAGAGATATTTATTTAAGTGCCTAGCTCGATA 525
QY 481 CATTAACGCCATTGACCATTCACCAATTTGGTGTGCACC 521
Db 526 CATTAACGCCATTGACCATTCACCAATTTGGTGTGCACC 566

RESULT 4
AAQ75973
ID AAQ75973 standard; cDNA; 4965 BP.
XX AC AAQ75973;
XX DT 25-MAR-2003 (revised)
XX DT 23-AUG-1995 (first entry)
XX DE pHLA-B7/beta-2 microglobulin expression vector.
XX KW expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7;
XX KW light beta-2 microglobulin; class I major histocompatibility complex;
XX KW MHC; bicistronic mRNA; human leukocyte antigen; HLA;
XX KW covalently closed circular DNA; ds.
XX OS Synthetic.
XX FH Key
XX FH LTR
XX FH Location/Qualifiers
XX FH 1. 529
XX FH /tag= a
XX FH /note= "Rous sarcoma virus LTR promoter domain, derived
XX FH for the Schmidt-Rupin strain nucleotides 8673-9146. This
XX FH region also includes a 56 bp region of a synthetic
XX FH oligonucleotide which modifies this regulatory sequence
XX FH to effect a higher level of expression of downstream
XX FH sequences. The oligonucleotide removes a polyadenylation
XX FH signal sequence originally found in the RSV DNA
XX FH sequence."
XX FH misc_signal
XX FH 531..534
XX FH /tag= b
XX FH /label= consensus_Kozak_signal_sequence
XX FH 535..1620
XX FH /tag= c
XX FH /note= "HLA-B7 heavy chain open reading frame"
XX FH 535..606
XX FH /tag= d
XX FH /note= "encodes putative signal peptide of the HLA-B7
XX FH heavy chain"
XX FH 607..1620

FT /tag= e
FT /note= "encodes putative HLA-B7 heavy chain mature
FT peptide"
FT 1621..1853
FT 3'UTR
FT /tag= f
FT /note= "3' untranslated sequence of HLA-B7 heavy chain
FT mRNA"
FT 1854..1888
FT misc_feature
FT /tag= g
FT /note= "multiple cloning site, forms a junction between
FT the HLA-B7 sequence and the EMCV-CITE sequence, and is
FT used to facilitate subcloning"
FT 1889..2479
FT RBS
FT /tag= h
FT /note= "murine encephalomyocarditis CAP-independent
FT translational enhancer (EMCV-CITE); taken from
FT nucleotides 255-843 of cloned EMCV genomic DNA. It is a
FT non-coding regulatory sequence functioning as an internal
FT entry point for the eukaryotic ribosomal subunits when
FT located within a mRNA mol. . It enables the translational
FT start codon of the beta-2 microglobulin, downstream of
FT the HLA-B7 stop codon on this bicistronic mRNA to be
FT recognised by the ribosome"
FT 2480..2839
FT CDS
FT /tag= i
FT /note= "encodes beta-2 microglobulin; this cDNA is deriv.
FT from chimpanzee (differs to the human cDNA by only 4
FT bases)"
FT 2840..2846
FT 3'UTR
FT /tag= j
FT /note= "3' untranslated region of the beta-2
FT microglobulin mRNA"
FT 2847..2870
FT misc_feature
FT /tag= k
FT /note= "synthetic linker"
FT 2879..2984
FT polyA_signal
FT /tag= l
FT 3112..3151
FT misc_feature
FT /tag= m
FT /note= "synthetic linker to facilitate cloning"
FT complement(3151..3967)
FT /tag= n
FT /note= "kanamycin resistance gene open reading frame; the
FT gene is taken from the transposable element Tn903"
FT 4014..4965
FT /tag= o
FT /note= "pBR322 backbone contg. bacterial origin of
FT replication, it represents nucleotides 2244-3193"
XX WO9429469-A2.
XX 22-DEC-1994.
XX 27-MAY-1994; 94WO-US006069.
XX 07-JUN-1993; 93US-00074344.
XX (VICA-) VICAL INC.
XX (UNMI) UNIV MICHIGAN.
XX Nabel GJ, Nabel EG, Lew D, Marquet M;
XX WPI; 1995-036494/05.
XX New vectors for gene therapy, partic for tumours - comprising genetic
XX material encoding one or more cistron(s) which express immunogenic or
XX therapeutic peptide(s).
XX Claim 8; Page 41-42; 50pp; English.
XX The pHLA-B7/beta-2 microglobulin plasmid expression vector, in addition
XX to the kanamycin resistance gene, contains the plasmid DNA encoding the
XX heavy (human HLA-B7) and light (beta-2 microglobulin) proteins of a class

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CC I major histocompatibility complex (MHC) antigen. The plasmid is  
 CC designed to express these two proteins via a bicistronic mRNA in  
 CC eukaryotic cells. Initiation of transcription of the mRNA is dependent on  
 CC a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long  
 CC terminal repeat. Termination of transcription is dependent upon the  
 CC polyadenylation signal sequence deriv. from the bovine growth hormone  
 CC gene. Eukaryotic cell translation of the heavy chain is regulated by the  
 CC 5' cap-dependent protein start site. Translation of the light chain is  
 CC controlled by the CITE. Finally the replication of the plasmid in  
 CC bacterial cells is controlled by the presence of a bacterial origin of  
 CC replication. The vector is used partic. for the treatment of neoplastic  
 CC disease, eg. melanoma, and provides enhanced gene delivery and expression  
 CC in vivo. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 4965 BP; 1171 A; 1293 C; 1338 G; 1163 T; 0 U; 0 Other;

Query Match 98.5%; Score 515; DB 2; Length 4965;  
 Best Local Similarity 99.0%; Pred. No. 3.4e-170;  
 Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGGACCAAAATTTAAGCTACA 60  
 DB 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGGACCAAAATTTAAGCTACA 60  
 QY 61 ACAAGCAAGGCTTGACCGACAAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTGG 120  
 DB 61 ACAAGCAAGGCTTGACCGACAAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTGG 120  
 QY 121 CTGCTTCGGATGTACGGGCGAGATTCGGGTATCTGAGGGAGTACGGTGTGTAGG 180  
 DB 121 CTGCTTCGGATGTACGGGCGAGATTCGGGTATCTGAGGGAGTACGGTGTGTAGG 180  
 QY 181 CGAAAACGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGGATATAGTGTTCGC 240  
 DB 181 CGAAAACGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGGATATAGTGTTCGC 240  
 QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTATGCAATCTCTGTGTAGTCTTGCACATGG 300  
 DB 241 TTTTGCATAGGAGGGGAAATCTAGTCTATGCAATCTCTGTGTAGTCTTGCACATGG 300  
 QY 301 TAACGATGATTTAGCAATGCTCTACAGGAGGAAAGACACCGTGCATGCGATGG 360  
 DB 301 TAACGATGATTTAGCAATGCTCTACAGGAGGAAAGACACCGTGCATGCGATGG 360  
 QY 361 TGGAGTAAAGTGTGTACGCTGTCTATTAGGAGGCAACAGACGGTCTGACATGGA 420  
 DB 361 TGGAGTAAAGTGTGTACGCTGTCTATTAGGAGGCAACAGACGGTCTGACATGGA 420  
 QY 421 TTGACGACACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAGTGCCTAGCTGATA 480  
 DB 421 TTGACGACACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAGTGCCTAGCTGATA 480  
 QY 481 CAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 DB 481 CTCTAGAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523

RESULT 5

ABZ23250

ID ABZ23250 standard; DNA; 562 BP.

XX AC

XX ABZ23250;

XX 24-MAR-2003 (first entry)

XX Nucleotide sequence of the Rous sarcoma virus (RSV)-LTR promoter.

XX p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production;  
 XX anchorage-independent producer cell line; ss.

XX Rous sarcoma virus.

XX WO200299100-A2.

XX 12-DEC-2002.  
 XX 03-JUN-2002; 2002WO-EP006054.  
 XX 01-JUN-2001; 2001GB-00013318.  
 XX (LONZ ) LONZA BIOLOGICS PLC.  
 XX Al-Rubeai M, Shuttleworth J;  
 XX WPI; 2003-148669/14.  
 XX Producing recombinant protein, particularly for maximizing or enhancing  
 XX e.g. therapeutic protein production, by co-expressing protein with  
 XX recombinant cell cycle inhibitor protein (p21) in producer cell line.  
 XX Disclosure; Page 32-33; 33pp; English.  
 XX The present sequence represents the Rous sarcoma virus (RSV)-LTR  
 XX promoter. The present sequence is used to produce vectors for use in the  
 XX method of the invention. The specification describes a method for  
 XX producing a protein, preferably a recombinant protein, in a mammalian  
 XX anchorage-independent producer cell line. The method comprises co-  
 XX expressing with the protein in the producer cell line a recombinant cell  
 XX cycle inhibitor protein (preferably p21). The method is useful for  
 XX producing a recombinant protein in a producer cell line. This is  
 XX particularly useful for maximizing or enhancing the production of e.g.  
 XX therapeutic proteins at an industrial scale

XX Sequence 562 BP; 143 A; 109 C; 163 G; 147 T; 0 U; 0 Other;

Query Match 98.2%; Score 513.8; DB 7; Length 562;  
 Best Local Similarity 99.6%; Pred. No. 2.9e-170;  
 Matches 515; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGGACCAAAATTTAAGCTACA 60  
 DB 46 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGGACCAAAATTTAAGCTACA 105  
 QY 61 ACAAGCAAGGCTTGACCGACAAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTGG 120  
 DB 106 ACAAGCAAGGCTTGACCGACAAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTGG 165  
 QY 121 CTGCTTCGGATGTACGGGCGGAGATTCGCTATCTGAGGGAGTACGGTGTGTAGG 180  
 DB 166 CTGCTTCGGATGTACGGGCGGAGATTCGCTATCTGAGGGAGTACGGTGTGTAGG 225  
 QY 181 CGAAAACGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGGATATAGTGTTCGC 240  
 DB 226 CGAAAACGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGGATATAGTGTTCGC 285  
 QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTATTGCAATCTCTGTGTAGTCTTGCACATGG 300  
 DB 286 TTTTGCATAGGAGGGGAAATCTAGTCTATTGCAATCTCTGTGTAGTCTTGCACATGG 345  
 QY 301 TAACGATGATTTAGCAACATCCCTTACAAGGAGGAAAGACCCGTGCATGCGATGG 360  
 DB 346 TAACGATGATTTAGCAACATCCCTTACAAGGAGGAAAGACCCGTGCATGCGATGG 405  
 QY 361 TGGAGTAAAGTGTGTACGCTGTCTATTAGGAGGCAACAGACGGTCTGACATGGA 420  
 DB 406 TGGAGTAAAGTGTGTACGCTGTCTATTAGGAGGCAACAGACGGTCTGACATGGA 465  
 QY 421 TTGACGACACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAGTGCCTAGCTGATA 480  
 DB 466 TTGACGACACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAGTGCCTAGCTGATA 525  
 QY 481 CAATAAACGCCATTGACCAATTCACCAATTTGGTGTG 517  
 DB 526 CAATAAACGCCATTGACCAATTCACCAATTTGGTGTG 562

RESULT 6  
 ADD35599  
 ID ADD35599 standard; DNA; 4457 BP.  
 XX  
 AC ADD35599;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Bicistronic eukaryotic expression vector PL178.  
 XX  
 KW Multicistronic eukaryotic expression vector; multiple protein expression;  
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;  
 KW chain terminator; transcription pause site; gene transfer;  
 KW DNA immunisation; gene therapy; PL178; kanamycin resistance gene;  
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;  
 KW hepatitis C virus; HCV IRES; mRSG terminator; cyclic; circular; ds.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 OS Rous sarcoma virus.  
 OS Cryptolagus cuniculus.  
 OS Hepatitis C virus.  
 OS Escherichia coli.  
 XX  
 XX WO2003031630-A1.  
 XX  
 XX 17-APR-2003.  
 XX  
 PF 10-OCT-2002; 2002WO-IT000646.  
 XX  
 XX 12-OCT-2001; 2001IT-MI002110.  
 XX  
 PA (KERY-) KERYOS SPA.  
 XX  
 PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;  
 XX  
 DR WPI; 2003-393446/37.  
 XX  
 XX New multicistronic recombinant plasmid vectors expressing two to our  
 PT genes simultaneously, useful in various biotechnological applications,  
 PT such as gene transfer, gene therapy and in DNA immunization.  
 XX  
 XX Claim 18; SEQ ID NO 2; 52pp; English.  
 XX  
 XX The invention relates to multicistronic eukaryotic expression vectors for  
 CC the expression of at least two proteins of interest which may be  
 CC identical or different. The vectors comprise at least one eukaryotic  
 CC expression cassette having a promoter/enhancer sequence, an intron  
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)  
 CC and a chain terminator. The vectors may additionally contain a  
 CC transcription pause site downstream of the chain terminator. The  
 CC invention also encompasses eukaryotic host cells comprising a vector of  
 CC the invention, and the recombinant expression of two or more eukaryotic  
 CC proteins using host cells transformed with a vector of the invention.  
 CC The vectors are useful in various biotechnological applications in which  
 CC the simultaneous expression of two or more genes is necessary, such as  
 CC gene transfer protocols, DNA immunisation, or for the expression of  
 CC different molecules in the same cell. They may also be used in gene  
 CC therapy. The present sequence represents a specifically claimed vector  
 CC designated PL178, which comprises a Rous sarcoma virus (RSV) promoter,  
 CC rabbit beta-globin intron, the hepatitis C virus (HCV) IRES, and a rabbit  
 CC beta-globin gene mRSG terminator as well as a kanamycin resistance gene.  
 XX  
 SQ Sequence 4457 BP; 1095 A; 1027 C; 1123 G; 1212 T; 0 U; 0 Other;  
 Query Match 97.3%; Score 508.8; DB 9; Length 4457;  
 Best Local Similarity 99.4%; Pred. No. 5e-168;  
 Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTGTGTGTGAGGTGCTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 457 CTGCTCCCTGCTGTGTGTGAGGTGCTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 516  
 Db

QY 61 ACAAGGCAAGGCTTCACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCGG 120  
 Db 517 ACAAGGCAAGGCTTCACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCGG 576  
 QY 121 CTGCTTCGGGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 577 CTGCTTCGGGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 636  
 QY 181 CGAAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
 Db 637 CGAAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 696  
 QY 241 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
 Db 697 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 756  
 QY 301 TTAAGTGTAGTGTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATCCGATTGG 360  
 Db 757 TTAAGTGTAGTGTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATCCGATTGG 816  
 QY 361 TGAAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAAGCAACAGACGGTCTGACATGA 420  
 Db 817 TGAAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAAGCAACAGACGGTCTGACATGA 876  
 QY 421 TTGACGACCAACCTAAATTCGCAATTCGACAGAT-ATTGTATTATTAGTGCCTAGCTGAT 479  
 Db 877 TTGACGACCAACCTAAATTCGCAATTCGACAGAT-ATTGTATTATTAGTGCCTAGCTGAT 936  
 QY 480 ACAATAAACGCCATTGACCATTCACCACATTTGGTGTGCACCTC 523  
 Db 937 ACAATAAACGCCATTGACCATTCACCACATTTGGTGTGCACCTC 980  
 RESULT 7  
 ADD35601/c  
 ID ADD35601 standard; DNA; 7334 BP.  
 XX  
 AC ADD35601;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Terracisronic eukaryotic expression vector PL250.  
 XX  
 KW Multicistronic eukaryotic expression vector; multiple protein expression;  
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;  
 KW chain terminator; transcription pause site; gene transfer;  
 KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;  
 KW cytomagalovirus; CMV promoter/enhancer; CMV intron A;  
 KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;  
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;  
 KW hepatitis C virus; HCV IRES; mRSG terminator; cyclic; circular; ds.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 OS Human herpesvirus 5.  
 OS Encephalomyocarditis virus.  
 OS Simian virus 40.  
 OS Rous sarcoma virus.  
 OS Cryptolagus cuniculus.  
 OS Hepatitis C virus.  
 OS Escherichia coli.  
 XX  
 XX WO2003031630-A1.  
 XX  
 XX 17-APR-2003.  
 XX  
 PF 10-OCT-2002; 2002WO-IT000646.  
 XX  
 XX 12-OCT-2001; 2001IT-MI002110.  
 XX  
 PA (KERY-) KERYOS SPA.  
 XX  
 PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;

XX DR WPI; 2003-393446/37.

XX PT New multicistronic recombinant plasmid vectors expressing two to our

XX PT genes simultaneously, useful in various biotechnological applications,

XX PT such as gene transfer, gene therapy and in DNA immunization.

XX PS Claim 18; SEQ ID NO 4; 52pp; English.

XX CC The invention relates to multicistronic eukaryotic expression vectors for

CC the expression of at least two proteins of interest which may be

CC identical or different. The vectors comprise at least one eukaryotic

CC expression cassette having a promoter/enhancer sequence, an intron

CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)

CC and a chain terminator. The vectors may additionally contain a

CC transcription pause site downstream of the chain terminator. The

CC invention also encompasses eukaryotic host cells comprising a vector of

CC the invention, and the recombinant expression of two or more eukaryotic

CC proteins using host cells transformed with a vector of the invention.

CC The vectors are useful in various biotechnological applications in which

CC the simultaneous expression of two or more genes is necessary, such as

CC gene transfer protocols, DNA immunisation, or for the expression of

CC different molecules in the same cell. They may also be used in gene

CC therapy. The present sequence represents a specifically claimed vector

CC designated PL250, which comprises a cytomegalovirus (CMV)

CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)

CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous

CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C

CC virus (HCV) IRES, and a rabbit beta-globin gene mGB terminator as well

CC as a kanamycin resistance gene.

XX SQ Sequence 7334 BP; 1922 A; 1775 C; 1825 G; 1812 T; 0 U; 0 Other;

Query Match 97.3%; Score 508.8; DB 9; Length 7334;

Best Local Similarity 99.4%; Pred. No. 6.4e-168;

Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAGTACA 60

Db 2300 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAGTACA 2241

Qy 61 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAAATCTGTAGGGTTAGCGGTTTGG 120

Db 2240 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAAATCTGTAGGGTTAGCGGTTTGG 2181

Qy 121 CTGCTTCGATGACGGGCGGCAATTCGCGTATCTGAGGCACTGAGGTGCTTTAG 180

Db 2180 CTGCTTCGATGACGGGCGGCAATTCGCGTATCTGAGGCACTGAGGTGCTTTAG 2121

Qy 181 CGAAAGCGGGCTTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240

Db 2120 CGAAAGCGGGCTTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 2061

Qy 241 TTTTGCATAGGAGGGGAATGATGCTTTATGCAATCTCTGAGTCTTGCACATGG 300

Db 2060 TTTTGCATAGGAGGGGAATGATGCTTTATGCAATCTCTGAGTCTTGCACATGG 2001

Qy 301 TAAAGTATGATAGCAATCGCTTACAAGGAGGAAAGACCGTGTGCGGATTGG 360

Db 2000 TAAAGTATGATAGCAATCGCTTACAAGGAGGAAAGACCGTGTGCGGATTGG 1941

Qy 361 TGGAGTATGATGATAGCAATCGCTTATAGGAGGCAACAGCGGTTGATGAGA 420

Db 1940 TGGAGTATGATGATAGCAATCGCTTATAGGAGGCAACAGCGGTTGATGAGA 1881

Qy 421 TTGAGCAACCACTAAATTCGCAATTCGCGAGAT-ATTGTATTAAAGTCCCTACTCGAT 479

Db 1880 TTGAGCAACCACTAAATTCGCAATTCGCGAGAT-ATTGTATTAAAGTCCCTACTCGAT 1821

Qy 480 ACAATTAACCCATTGTACCAATTCACCAATTTGGTGGCACCTC 523

Db 1820 ACAATTAACCCATTGTACCAATTCACCAATTTGGTGGCACCTC 1777

RESULT 8

AAQ75974/C

ID AAQ75974 standard; cDNA; 4059 BP.

XX AC AAQ75974;

XX DT 25-MAR-2003 (revised)

XX DT 23-AUG-1995 (first entry)

XX DE pHLA-B7 expression vector.

XX KW expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;

XX KW light beta-2 microglobulin; class I major histocompatibility complex;

XX KW MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.

XX OS Synthetic.

XX Key Location/Qualifiers

FT misc\_feature 1..354

FT /tag= a

FT /note= "pBR322 backbone contg. bacterial origin of

FT replication"

FT 355..1170

FT /tag= b

FT /note= "kanamycin resistance gene open reading frame; the

FT gene is taken from the transposable element Tn903"

FT polyA\_signal

FT /tag= c

FT /note= "SV40 polyA signal sequence"

FT complement(1412..1560)

FT /tag= d

FT /note= "SV40 small t intron"

FT /tag= e

FT complement(1561..1794)

FT /tag= f

FT /note= "3' untranslated region of HLA-B7 heavy chain

FT mRNA"

FT complement(1795..2880)

FT /tag= f

FT /note= "HLA-B7 open reading frame"

FT complement(2886..3415)

FT /tag= g

FT /note= "Rous sarcoma virus 3' LTR promoter region"

FT 3416..4059

FT /tag= h

FT /note= "pBR322 backbone"

XX W09429469-A2.

XX DT 22-DEC-1994.

XX PF 27-MAY-1994; 94WO-US006069.

XX PR 07-JUN-1993; 93US-00074344.

XX PA (VICA-) VICAL INC.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Nabel GJ, Nabel EG, Lew D, Marquet M;

XX DT WPI; 1995-036494/05.

XX New vectors for gene therapy, partic for tumours - comprising genetic

PT material encoding one or more cistron(s) which express immunogenic or

PT therapeutic peptide(s).

XX Claim 9; Page 42-43; 50pp; English.

XX This HLA-B7 antigen encoding plasmid was developed to incorporate many

CC advantageous features, eg. the kanamycin resistance gene. The

CC eradication of two open reading frames encoding portions of SV40 viral

CC proteins lowers the risk of tumorigenicity. The vector may also operate

CC as a cassette into which cistrons may be inserted and removed at will for

CC the transcription and subsequent translation of peptides of interest. The  
 CC vector is used partic. for the treatment of neoplastic disease, eg.  
 CC melanoma, and provides enhanced gene delivery and expression in vivo.  
 CC (updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 U; 0 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 4059;  
 Best Local Similarity 99.0%; Pred. No. 6.3e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTTGGAGGCTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 60  
 Db 3415 CTGCTCCCTGCTGTTGGAGGCTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 3356

QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGTTAGGCTTAGCGTTTGGG 120

Db 3355 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGTTAGGCTTAGCGTTTGGG 3296

QY 121 CTGCTTCGATGTAGCGGCCAGATATTCGCGTATCTAGGAGGCTAGGTTGTTAGG 180

Db 3295 CTGCTTCGATGTAGCGGCCAGATATTCGCGTATCTAGGAGGCTAGGTTGTTAGG 3236

QY 181 CGAAAGCGGGCTTCGCTTGTAGCGGTTAGAGTCCCTCAGGATATAGTACTTCCG 240

Db 3235 CGAAAGCGGGCTTCGCTTGTAGCGGTTAGAGTCCCTCAGGATATAGTACTTCCG 3176

QY 241 TTTTGCATAGGAGGGGAAATGATGCTTATGCAATCTTGTAGTCTTGCAACATGG 300

Db 3175 TTTTGCATAGGAGGGGAAATGATGCTTATGCAATCTTGTAGTCTTGCAACATGG 3116

QY 301 TAACGATGATGTAGCAACATGCCCTTACAGGAGAGAAAGCAACCTGATGCCGATTGG 360

Db 3115 TAACGATGATGTAGCAACATGCCCTTACAGGAGAGAAAGCAACCTGATGCCGATTGG 3056

QY 361 TGGAGTAAAGTGGTACGATCGCTTATAGGAGGCAACAGCGGCTCTGACATGGA 420

Db 3055 TGGAGTAAAGTGGTACGATCGCTTATAGGAGGCAACAGCGGCTCTGACATGGA 2996

QY 421 TTGAGCAACACCTAAATTCGCGCATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479

Db 2995 TTGAGCAACACCTAAATTCGCGCATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 2936

QY 480 ACAATPAAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523

Db 2935 ACAATPAAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 2892

RESULT 9

ID AAQ62391 standard; DNA; 4341 BP.

XX AC AAQ62391;

DT 25-MAR-2003 (revised)

DT 18-NOV-1994 (first entry)

DE Vector pVAC1.

XX Vector; pVAC1; pRC/RSV; leader sequence; termination signal;

KW fusion protein; pSfi/Not.Tag1; pElB leader; human; immunoglobulin; VHL;

KW single chain; Fv; murine antibody; retroviral; envelope; plasmid;

KW vaccine; ss.

XX Synthetic.

XX Key Location/Qualifiers

PH Complement (1..775)

FT misc\_RNA

FT /\*tag= c

FT /note= "Claim 9"

FT misc\_RNA

FT /\*tag= b

FT /note= "Claim 8"

FT misc\_RNA 606..716  
 FT /\*tag= a  
 FT /note= "Claim 7"

XX WO9408008-A1.

XX PD 14-APR-1994.

XX PF 04-OCT-1993; 93WO-GB002054.

XX PR 02-OCT-1992; 92GB-00020808.

XX PA (MEDI-) MEDICAL RES COUNCIL.

XX PI Hawkins RE, Russell SJ, Stevenson FK, Winter GP;

XX DR WPI; 1994-135575/16.

XX Modulating immune response to a disease marker - by administering a  
 PT vector which expresses the disease marker to interact with the immune  
 PT system.

XX Claim 10; Fig 7; 77pp; English.

XX This sequence represents the vector pVAC1. This vector is based on the  
 CC commercially available vector pRC/RSV. Leader sequences and termination  
 CC signals were introduced into the vector to allow for production of fusion  
 CC proteins. The vector, pSfi/Not.Tag1, was modified to replace the pElB  
 CC leader with the human immunoglobulin VHL leader sequence that permits the  
 CC encoding of an sfil cloning site without modification of the amino acid  
 CC sequence. This fragment was then cloned as an EcoRI/Bln-HindIII  
 CC fragment into NotI/Bln-HindIII cut vector pRC/RSV to give pVAC1. The  
 CC single chain Fv for an individual patient can be inserted within the VHL  
 CC leader sequence. This plasmid when encoding a single chain murine  
 CC antibody/retroviral envelope fusion protein can be used as a plasmid  
 CC vaccine and it induces a strong humoral response to the antibody moiety  
 CC in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 4341;

Best Local Similarity 99.0%; Pred. No. 6.6e-167;

Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTTGGAGGCTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 60

Db 81 CTGCTCCCTGCTGTTGGAGGCTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGGTTAGCGTTTTCG 120

Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGGTTAGCGTTTTCG 200

QY 121 CTGCTTCGATGTAGCGGCCAGATATTCGCGTATCTAGGAGGCTAGGTTGTTAGG 180

Db 201 CTGCTTCGATGTAGCGGCCAGATATTCGCGTATCTAGGAGGCTAGGTTGTTAGG 260

QY 181 CGAAAGCGGGCTTCGCTTGTAGCGGTTAGAGTCCCTCAGGATATAGTACTTCCG 240

Db 261 CGAAAGCGGGCTTCGCTTGTAGCGGTTAGAGTCCCTCAGGATATAGTACTTCCG 320

QY 241 TTTTGCATAGGAGGGGAAATGATGCTTATGCAATCTTGTAGTCTTGCAACATGG 300

Db 321 TTTTGCATAGGAGGGGAAATGATGCTTATGCAATCTTGTAGTCTTGCAACATGG 380

QY 301 TAACGATGATGTAGCAACATGCCCTTACAGGAGAGAAAGCAACCTGATGCCGATTGG 360

Db 381 TAACGATGATGTAGCAACATGCCCTTACAGGAGAGAAAGCAACCTGATGCCGATTGG 440

QY 361 TGGAGTAAAGTGGTACGATCGCTTATAGGAGGCAACAGCGGCTCTGACATGGA 420

Db 441 TGGAGTAAAGTGGTACGATCGCTTATAGGAGGCAACAGCGGCTCTGACATGGA 500

QY 421 TTGAGCAACACCTAAATTCGCGCATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479

Db 501 TTGGACGACCACTGAAATTCGGATTTCGAGAGATAATTTGTTAAGTGCTAGTCGAT 560  
 QY 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGTCGACCTC 523  
 Db 561 ACAATAAGCCATTGACCAATTCACCAATTCGATGTCGACCTC 604

RESULT 10  
 AAS17704  
 ID AAS17704 standard; DNA; 4341 BP.  
 AC AAS17704;  
 DT 12-MAR-2002 (first entry)  
 XX Vector pVAC1 encoding a DNA vaccine.  
 DE Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;  
 KW Clostridium tetani.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Cauliflower mosaic virus.  
 XX WO200179510-A1.  
 XX 25-OCT-2001.  
 XX 17-APR-2001; 2001WO-GB001719.  
 XX 17-APR-2000; 2000GB-00009470.  
 XX (CANC-) CANCER RES VENTURES LTD.  
 XX Rice J, Stevenson F;  
 XX WPI; 2002-066370/09.  
 XX Nucleic acid construct, useful to immunize against various diseases  
 PT including cancer, expresses the first domain of tetanus toxin FrC fused  
 PT to a disease peptide antigen to provide a vaccine.  
 XX Disclosure; Fig 4; 71pp; English.  
 XX The invention relates to a nucleic acid construct for delivery into  
 CC living cells in vivo, to induce an immune response to a disease peptide  
 CC antigen, where the construct directs expression of a fusion protein  
 CC comprising the peptide antigen and the first domain of FrC. Also included  
 CC are a nucleic acid vector comprising the above construct, a host cell  
 CC comprising the above construct or vector and a method of producing a  
 CC nucleic acid construct for inducing an immune response. The method  
 CC comprises identifying a nucleic acid sequence encoding a disease peptide  
 CC antigen comprising epitopes characteristic of the disease, cloning the  
 CC nucleic acid sequence, introducing the cloned nucleic acid into a vector  
 CC which allows the antigen to be expressed as a fusion with a first domain  
 CC FrC from tetanus toxin, and optionally isolating the construct from the  
 CC vector. The construct or vector is used as a vaccine to induce an immune  
 CC response, particularly to tumour antigens. The present sequence is vector  
 CC pVAC1 which encodes a vaccine of the invention  
 XX Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;  
 SQ

Query Match 96.7%; Score 505.6; DB 6; Length 4341;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTGTGTGTTGGAGTGGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGACCGACAAATTCGATGAAGAAATCTGCTTAGGGTTAGGGCTTTGGC 120

Db 141 ACAAGGCAAGGCTTGACCGACAAATTCGATGAAGAAATCTGCTTAGGGTTAGGGCTTTGGC 200  
 QY 121 CTGCTCCCTGCGATGACGGGCGAGATATTCGGCTATCTGAGGGACTAGGGTGTCTTTAGG 180  
 Db 201 CTGCTCCCTGCGATGACGGGCGAGATATTCGGCTATCTGAGGGACTAGGGTGTCTTTAGG 260  
 QY 181 CGAAAGCGGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
 Db 261 CGAAAGCGGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 320  
 QY 241 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGG 300  
 Db 321 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGG 380  
 QY 301 TAAAGATGAGTTAGCAATCGCTTCAAGGAGAGAAAGACCCGTGCATGCCGATTTGG 360  
 Db 381 TAAAGATGAGTTAGCAATCGCTTCAAGGAGAGAAAGACCCGTGCATGCCGATTTGG 440  
 QY 361 TGAAGTAAAGTGGTACGATCGTGCCTTTATTAGGAGGCAACAGCGGTCTGCATGGA 420  
 Db 441 TGAAGTAAAGTGGTACGATCGTGCCTTTATTAGGAGGCAACAGCGGTCTGCATGGA 500  
 QY 421 TTGACGAGACCACTAAATTCGCAATTCGAGAT-ATTGTATTATTAGTGCCTAGCTCGAT 479  
 Db 501 TTGACGAGACCACTAAATTCGCAATTCGAGATATTGTATTATTAGTGCCTAGCTCGAT 560  
 QY 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGTCGACCTC 523  
 Db 561 ACAATAAGCCATTGACCAATTCACCAATTCGATGTCGACCTC 604

RESULT 11  
 AEN83143  
 ID AEN83143 standard; DNA; 4341 BP.  
 XX AEN83143;  
 XX 10-SEP-2002 (first entry)  
 XX Plasmid pVAC1 complete sequence.  
 XX Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;  
 KW cancer; B cell malignancy; ds.  
 XX Synthetic.  
 XX WO200240513-A2.  
 XX 23-MAY-2002.  
 XX 20-NOV-2001; 2001WO-GB005142.  
 XX 20-NOV-2000; 2000GB-00028319.  
 XX (CANC-) CANCER RES VENTURES LTD.  
 XX Savel'yeva N, Stevenson F;  
 XX WPI; 2002-500202/53.  
 XX Nucleic acid construct for delivery into living cells as a vaccine,  
 PT useful for treating e.g. cancer, directs the expression of a fusion  
 PT protein comprising an antigen and an adjuvant sequence derived from a  
 PT plant viral coat protein.  
 XX Example 3; Fig 7; 84pp; English.  
 XX The invention relates to a novel nucleic acid construct for inducing an  
 CC immune response in vivo to an antigen, capable of directing the  
 CC expression of a fusion protein that comprises an antigen and an adjuvant  
 CC sequence derived from a plant viral coat protein. The construct of the  
 CC invention has cytostatic and virucide activity. The nucleic acid

CC construct is useful for inducing an immune response in a patient, for  
CC vaccinating a patient against an infectious disease caused by an antigen.  
CC derived from a pathogen e.g. a virus, for treating a cancer patient or a  
CC patient with a predisposition to cancer and for treating a patient having  
CC a B cell malignancy, where the construct is encapsidated, and optionally,  
CC a second nucleic acid sequence encoding a further immunomodulatory  
CC polypeptide is administered to the patient. The construct is also useful  
CC in medical treatment, and in the preparation of a vaccine for treating or  
CC preventing a disease state associated with the antigen. The sequence  
CC shows the complete sequence of vector pVAC1  
XX  
SQ Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;  
Query Match 96.7%; Score 505.6; DB 6; Length 4341;  
Best Local Similarity 99.0%; Pred. No. 6.6e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTGTGGCGAGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTGTGGCGAGCAAAATTAAGCTACA 140  
QY 61 ACAGGCAAGGCTTGACCGCAATTCATGAGAAATCTGCTTAGGGTTAGCGCTTTGGC 120  
Db 141 ACAGGCAAGGCTTGACCGCAATTCATGAGAAATCTGCTTAGGGTTAGCGCTTTGGC 200  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 201 CTGCTTCGCGATGTACGGGCCAGATATTCGGCTATCTGAGGGGACTAGGGTGTGTTAGG 260  
QY 181 CGAAAGCGGGCTTCGGTGTGTGACGGGTTAGGAGTCCCTCAGGATATAGATTTCGC 240  
Db 261 CGAAAGCGGGCTTCGGTGTGTGACGGGTTAGGAGTCCCTCAGGATATAGATTTCGC 320  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
Db 321 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 380  
QY 301 TAACGATGATGTAGCAACATGCCCTTACAAGGAGAGAAAGACCGTGATGCCGATTTGG 360  
Db 381 TAAAGGATGTAGCAACATGCCCTTACAAGGAGAGAAAGACCGTGATGCCGATTTGG 440  
QY 361 TGGAGTGTAGGTTGATGATCGTGCCTTATTAGGAGGCAACAGCGGTCTGACATGGA 420  
Db 441 TGGAGTGTAGGTTGATGATCGTGCCTTATTAGGAGGCAACAGCGGTCTGACATGGA 500  
QY 421 TTGACCAACCACTAAATTCGCATTCGACAGAT -ATTGTATTTAAGTCCCTAGCTCGAT 479  
Db 501 TTGACCAACCACTAAATTCGCATTCGACAGATTTATTTAAGTCCCTAGCTCGAT 560  
QY 480 ACAATAAACGCCATTGTACCATTCACACATTTGGTGTGCACCTC 523  
Db 561 ACAATAAACGCCATTGTACCATTCACACATTTGGTGTGCACCTC 604  
RESULT 12  
AA02998  
ID AA02998 standard; DNA; 5653 BP.  
XX  
AC AA02998;  
XX  
DT 24-MAR-1996 (first entry)  
XX  
DE RSV tar Rev M10 expression plasmid pRSVRevM10.  
XX  
KW Plasmid pRSVRevM10; particle-mediated gene transfer; cyc.i.c;  
KW particle acceleration; HIV virus infection; gene therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..36  
FT /\*tag= a  
FT /\*note= "pBR322 vector sequence"

FT enhancer 37..610  
FT /\*tag= b  
FT /\*note= "RSV enhancer"  
FT promoter 611..699  
FT /\*tag= c  
FT /\*label= tar  
FT /\*note= "HIV promoter tat responsive element"  
FT mat\_peptide 700..1129  
FT /\*tag= d  
FT /\*note= "Rev M10 open reading frame"  
FT polyA\_signal 1243  
FT /\*tag= e  
FT /\*note= "cattle somatotropin poly(A) site"  
FT promoter 1993..2300  
FT /\*tag= f  
FT /\*note= "pSVneo promoter"  
FT misc\_feature 2346  
FT /\*tag= g  
FT /\*label= kanamycin\_resistance\_gene  
FT /\*note= "pSV2 neo selectable marker gene"  
FT polyA\_signal 3360  
FT /\*tag= h  
FT /\*note= "pSV2 neo"  
FT misc\_feature 3459..5653  
FT /\*tag= i  
FT /\*note= "plasmid pUC ori/amp sequence"  
XX  
XX WO9529703-A1.  
PN 09-NOV-1995.  
XX  
XX 01-MAY-1995; 95WO-US005024.  
XX  
XX 29-APR-1994; 94US-00235277.  
XX (NABE/) NABEL G J.  
XX (WOFF/) WOFFENDIN C.  
XX (YANG/) YANG N.  
XX (SHEE/) SHEEHY M J.  
PI Nabel GU, Woffendin C, Yang N, Sheehy MJ;  
XX  
XX WPI; 1995-403807/51.  
XX  
XX Particle-mediated gene transfer - in T cells, monocytes, macrophage(s),  
PT dendrites or haematopoietic stem cells, partic. for treating HIV  
PT infection.  
XX  
XX Disclosure; Fig 11a-11e; 96pp; English.  
XX  
XX Expression plasmid pRSVRevM10 contains the Rev M10 HIV protective gene  
CC (a dominant-negative inhibition gene) under the control of the Tar  
CC sequence (HIV promoter -18 to -72), i.e. gene expression is activated by  
CC Tat. The plasmid also contains the kanamycin-resistance selectable  
CC marker gene. The plasmid is used in a particle-mediated gene transfer  
CC process for Rev M10 gene expression in T-cells (preferably), monocytes,  
CC macrophages, haematopoietic stem cells or dendrites. The gold  
CC microparticle acceleration process results in stable incorporation of  
CC foreign genes in the cells. This method is used to treat HIV infection.  
CC Rev M10 transduced cells are resistant to HIV challenge. The method may  
CC be applied to the transfer of other therapeutic genes in a gene therapy  
CC process  
XX  
XX Sequence 5653 BP; 1328 A; 1428 C; 1478 G; 1419 T; 0 U; 0 Other;  
SQ  
Query Match 96.7%; Score 505.6; DB 2; Length 5653;  
Best Local Similarity 99.0%; Pred. No. 7.5e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTGTGGCGAGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTGTGGCGAGCAAAATTAAGCTACA 140





QY	301	TTAACGATGAGTTAGCAACAATGCTTTACAAAGGAGAGAAAAAGCACCGTGCATGCCGATTGG	360
Db	381	TAAACGATGAGTTAGCAACAATGCTTTACAAAGGAGAGAAAAAGCACCGTGCATGCCGATTGG	440
QY	361	TGGAGTAAGGTGGTACGATCGTGCCTTATTAGGAGGCAACGACGGGTCTGCATGGA	420
Db	441	TGGAAGTAAGGTGGTACGATCGTGCCTTATTAGGAGGCAACGACGGGTCTGCATGGA	500
QY	421	TTGGAGCAACCACTAAATTCGCAATTGCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT	479
Db	501	TTGGAGCAACCACTAAATTCGCAATTGCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT	560
QY	480	ACAATAAAGCGCAATTGACCAATTCACCACTTGGTGTGACACCTC	523
Db	561	ACAATAAAGCGCAATTGACCAATTCACCACTTGGTGTGACACCTC	604
RESULT 15			
AAQ43813			
ID AAQ43813 standard; DNA; 6207 BP.			
XX	AC	AAQ43813;	
XX	AC	AAQ43813;	
DT	25-MAR-2003	(revised)	
DT	20-OCT-1993	(first entry)	
XX	XX		
DE	XX	pRLD2D3D4 construct.	
XX	XX		
KW	XX	Epidermal growth factor receptor truncate protein; EGF; binding sites;	
KW	XX	adsorptive agents; mammalian cell growth abnormality; detection; growth;	
KW	XX	reproduction; signal transmission; ds.	
XX	XX		
XX	XX	Synthetic.	
XX	XX		
Key	XX	Location/Qualifiers	
FT	XX	665..2193	
CDS	XX	/*tag= a	
FT	XX	/codon= 707-708 CG encodes Ile	
FT	XX	/note= "encodes LD2D3D4"	
FT	XX	1519..1521	
FT	XX	/*tag= b	
FT	XX	/note= "codon ARA encodes Ile"	
XX	XX		
FN	XX	US5218090-A.	
XX	XX		
PD	XX	08-JUN-1993.	
XX	XX		
PF	XX	26-OCT-1990; 90US-00604728.	
XX	XX		
PR	XX	12-JUN-1990; 90US-00536896.	
XX	XX		
PA	XX	(WARN ) WARNER LAMBERT CO.	
XX	XX		
PI	XX	Connors RW;	
XX	XX		
DR	XX	WPI; 1993-196297/24.	
DR	XX	P-PSDB; AAR38210.	
XX	XX		
PT	XX	New epidermal growth factor receptor truncate proteins - which bind	
PT	XX	ligands of EGF receptor without transmitting signal for growth or	
PT	XX	reproduction.	
XX	XX		
PS	XX	Disclosure; Fig 6; 42pp; English.	
XX	XX		
CC	XX	The sequence is that of the pRLD2D3D4 construct which encodes the	
CC	XX	epidermal growth factor (EGF) receptor truncate protein LD2D3D4 having	
CC	XX	EGF binding sites. The protein binds ligands of the EGF receptor without	
CC	XX	transmitting a signal for the growth and reproduction of a cell. It can	
CC	XX	be used as an adsorptive agent for any moieties that bind the EGF	
CC	XX	receptor as the portal of entry to a cell. It competes with the EGF	
CC	XX	receptor present on the cell surface for the binding of ligands and	
CC	XX	thereby inhibits the action of the ligands or prevents the entry of	

CC viruses into cells. It can also be used as for the EGF receptor itself.  
CC such as in the detection of abnormalities in mammalian cell growth. It is  
CC also useful for prepreg. novel receptors for efficient detection of ligands  
CC and their anti-agonists or agonists. The features table indicates the  
CC discrepancies between the L2D23D4 protein sequence given in the  
CC specification and that which the PR1D2D34 DNA sequence given in the  
CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
XX Sequence 6207 BP: 1474 A; 1620 C; 1670 G; 1442 T; 0 U; 1 Other;  
SO

Query Match 96.7%; Score 505.6; DB 2; Length 6207;  
Best Local Similarity 99.0%; Pred. No. 7.9e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY	1	CTCTCCCTCCCTGCTGTGTGTGGAGGTGCGCTAGCTAGTGC	CGAGCAAAATTTAGCTACA	60
DB	81	CTCTCCCTCCCTGCTGTGTGTGGAGGTGCGCTAGCTAGTGC	CGAGCAAAATTTAGCTACA	140
QY	61	ACAAGCGAAGGCTTGCACGACAATTGCATGAAGAAATCGCTT	TAGGGTTAGCGCTTTTGG	120
DB	141	ACAAGCGAAGGCTTGCACGACAATTGCATGAAGAAATCGCTT	TAGGGTTAGCGCTTTTGG	200
QY	121	CTGCTTCGGGATGTACGGGCGAGATATTCGCGTATCTCAGG	GGAAGCTAGGGTGTCTTTAGG	180
DB	201	CTGCTTTCGGGATGTACGGGCGAGATATTCGCGTATCTCAGG	GGAAGCTAGGGTGTCTTTAGG	260
QY	181	CGAAAAAGCGGGGCTTCGGTTGTACCGCGTTTAGGAGTCCCT	TCAGGATATAGTAGTTTCGC	240
DB	261	CGAAAAAGCGGGGCTTCGGTTGTACCGCGTTTAGGAGTCCCT	TCAGGATATAGTAGTTTCGC	320
QY	241	TTTTCGATAGGAGAGGGGAAATGTATAGTCTTATGCAATACT	CTTGTGTAGTCTTGCACATGG	300
DB	321	TTTTCGATAGGAGAGGGGAAATGTATAGTCTTATGCAATACT	CTTGTGTAGTCTTGCACATGG	380
QY	301	TTACGATAGGTTTACCAATGCTCTTACAAGGAGAGAAAAAGCA	CCGTCGATGCCGCAATGG	360
DB	381	TACGATAGGTTTACCAATGCTCTTACAAGGAGAGAAAAAGCA	CCGTCGATGCCGCAATGG	440
QY	361	TGGAAGTAAAGTGGTACGATCGTGCTTTATTAGGAAGGCAAC	AGACGGGCTGTGACATGGA	420
DB	441	TGGAAGTAAAGTGGTACGATCGTGCTTTATTAGGAAGGCAAC	AGACGGGCTGTGACATGGA	500
QY	421	TTTGAAGAACCACTAAATTCGGCATTCGAGAGAT-ATTGTATT	TTTAAAGTGCCTAGCTCGAT	479
DB	501	TTTGAAGAACCACTAAATTCGGCATTCGAGAGAT-ATTGTATT	TTTAAAGTGCCTAGCTCGAT	560
QY	480	ACAAATAAAGCCCATTTGACCATTCACCAATTCGGTGTGACCTC		523
DB	561	ACAAATAAAGCCCATTTGACCATTCACCAATTCGGTGTGACCTC		604

RESULT 16	
AAQ43812	
ID	AAQ43812 standard; DNA; 6274 BP.
XX	
AC	AAQ43812;
XX	
DT	25-MAR-2003 (revised)
DT	20-OCT-1993 (first entry)
XX	
DE	pRLD1D2D3.Apal construct.
XX	
KW	Epidermal growth factor receptor truncate protein; EGF; growth;
KW	binding sites; adsorptive agents; mammalian cell growth abnormality;
KW	defection. reproduction. signal transmission. pRLD1D2D3Apal; ds.

XX	Key	Location/Qualifiers
PH	CDS	665..2253
FT		/*tag= a
FT		/codon= 707-708 CG encodes Ile
FT		/note= "encodes LD1D23ApaL"

```

PT misc_feature 1939..1941
FT /**tag= b
PT /note= "codon ARA encodes Ile"
XX
XX
XX US5218090-A.
XX PN
XX XX
XX XX
XX 08-JUN-1993.
XX PD
XX XX
XX 26-OCT-1990; 90US-00604728.
XX PF
XX XX
XX 12-JUN-1990; 90US-00536896.
XX PR
XX XX
XX (WARN ) WARNER LAMBERT CO.
XX PA
XX XX
XX Connors RW;
XX PI
XX XX
XX WPI; 1993-196297/24.
XX DR
XX P-PSDB: AAR38209.
XX DR

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New epidermal growth factor receptor truncate proteins - which bind ligands of EGF receptor without transmitting signal for growth or reproduction.

Disclosure: Fig 3: 42pp: English.

The sequence is that of the pRL1D2D3 construct which encodes the epidermal growth factor (EGF) truncate protein L1D1D2D3Δpal having EGF binding sites. The protein binds ligands of the EGF receptor without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any moieties that bind the EGF receptor as the portal of entry to a cell. It competes with the EGF receptor present on the cell surface for the binding of ligands and thereby inhibits the action of the ligands or prevents the entry of viruses into cells. It can also be used as for the EGF receptor itself, such as in the detection of abnormalities in mammalian cell growth. It is also useful for prep99. novel receptors for efficient detection of ligands and their anti-agonists or agonists. The features table indicates the discrepancies between the L1D1D2D3 protein sequence given in the specification and that which the pRL1D1D2D3 DNA sequence given in the specification would encode. (Updated on 25-MAR-2003 to correct PF field.)

Sequence	6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 0 U; 1 Other;
Every Match	96.7%; Score 505.6; DB 2; Length 6274;
Fast Local Similarity	99.0%; Pred. No. 8e-167;
Matches 519: Conservative	0; Mismatches 4; Indels 1; Gaps 1

QY	1	CTGCTCCCTCTGTGTGTGGAGTCGCTGAGTAGTGGCGGAGCAAAATTTAAAGCTACA	50
Db	81	CTGCTCCCTCTGTGTGTGGAGTCGCTGAGTAGTGGCGGAGCAAAATTTAAAGCTACA	140
QY	61	ACAGGGCAGGCTTGACCGACAATGTCATCAAGAAATCTGCTTAGGGTTAGCGTTTTCGG	120
Db	141	ACAAGGCAAGCTTTGACCGACAAATGCAATGAAGAAATCTGCTTAGGGTTAGCGTTTTCGG	200
QY	121	CTGCTTCGCAATGACGGCCAGATATTCGCTATCTCAGGGGACTAGGGTGCTTTTAGG	180
Db	201	CTGCTTCGCAATGACGGCCAGATATPACGCGTATCTGAGGGGACTAGGGTGCTTTTAGG	260
QY	181	CGAAAGCGGGGCTTCGGTTGTACCGGTTTAGAGTCCCTTCAGGATATAGTAGTTTCGC	240
Db	261	CGAAAGCGGGGCTTCGGTTGTACCGGTTTAGAGTCCCTTCAGGATATAGTAGTTTCGC	320
QY	241	TTTTGCATAGGAGGGGGAAATGTAGTCCTATGCAATCTCTTGTGTAGCTTCGCAACATGG	300
Db	321	TTTTGCATAGGAGGGGGAAATGTAGTCCTATGCAATACATTTGTAGTCTGCAACATGG	380
QY	301	TAAAGATGAGTTAGCAACATGCTCTTACAAGGAGGAAAAACCGCTGCATGCCGATGG	360
Db	381	TAAAGATGAGTTAGCAACATGCTCTTACAAGGAGGAAAAACCGCTGCATGCCGATGG	440
QY	361	TGGAAGTAAAGTGGTACGATCGTCGCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA	420

Db 441 TGGAGTAAAGTGGTACGATCGTCTTATTAGGAGGCAACAGACAGGTCTGACATGGA 500  
 Qy 421 TTGGACGACCACTAAATTCGGATTCGAGAGAT-ATTGTAATTTAACTGCGCTAGCTCGAT 479  
 Db 501 TTGGACGACCACTGAATTCGGATTCGAGAGATATTGTAATTTAACTGCGCTAGCTCGAT 560  
 Qy 480 ACATTAAGCCATTTGACCATTCACACATTTGGTGGCACCTC 523  
 Db 561 ACATTAAGCCATTTGACCATTCACACATTTGGTGGCACCTC 604

RESULT 17

AAT84562  
 ID AAT84562 standard; cDNA; 8591 BP.  
 AC AAT84562;  
 XX 25-MAR-2003 (revised)  
 DT 15-DEC-1997 (first entry)  
 XX Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;  
 KW mutelin; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;  
 KW cyclic.

XX Homo; sapiens.  
 OS Synthetic.  
 OS Chimeric.

PH Key Location/Qualifiers  
 FT CDS 2393..3856  
 FT /\*tag= a

XX U85652092-A.  
 XX 29-JUL-1997.

XX 05-JUN-1995; 95US-00462859.  
 XX 01-MAY-1992; 92US-00877675.  
 PR 20-SEP-1993; 93US-00123659.

XX (AMCY ) AMERICAN CYANAMID CO.  
 XX Jacobsen JS, Vitek MP;  
 XX WPI; 1997-392937/36.  
 DR P-PSDB; AAW26394.

XX Screening for compounds which reduce beta-amyloid protein formation -  
 PT using cells which express a construct encoding a marker and an amyloid  
 PT precursor mutelin derived from APP isoforms.  
 XX Disclosure; Fig 8; 84pp; English.

XX Plasmid pCLL621 (AAT84562), deposited in E. coli as ATCC 69406, codes  
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751  
 CC (see AAW26394), that has a 276-amino acid deletion of the native APP and  
 CC carries a Substance P epitope marker on the N-terminal side of the beta-  
 CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method  
 CC for screening for a compound which reduces the formation of beta-amyloid  
 CC protein, determined by measuring the amount of marker in a medium  
 CC containing transfected cells. The method is used to detect compounds  
 CC which inhibit the activity of proteolytic enzymes which cleave APP to  
 CC generate BAP fragments. Such compounds can be used in the treatment of  
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP  
 CC distinguishes the construct from endogenously expressed APP, and  
 CC beneficially increases the resolution of APP-REP fragments resulting from  
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-  
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
 Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTCTTGTGTGCTTGGAGTTCGCTGAGTTCGCGAGCAAAATTTAAGCTACA 60  
 Db 4716 CTGCTCCCTCTTGTGTGCTTGGAGTTCGCTGAGTTCGCGAGCAAAATTTAAGCTACA 4775

Qy 61 ACAAGGCAGGCTTGACGCAATTCATGAAGAATCTGCTTAGGGTTAGGCTTTTGGC 120  
 Db 4776 ACAAGGCAGGCTTGACGCAATTCATGAAGAATCTGCTTAGGGTTAGGCTTTTGGC 4835

Qy 121 CTGCTTCGATGATACGGGCGAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 180  
 Db 4836 CTGCTTCGATGATACGGGCGAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 4895

Qy 181 CGAAAAGCGGGGCTTCGGTTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTGCG 240  
 Db 4896 CGAAAAGCGGGGCTTCGGTTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTGCG 4955

Qy 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db 4956 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

Qy 301 TAACTGATGTTAGCAACATGCTTACAAGAGAGAAAAGCAGCCGTGCATGCCATTGG 360  
 Db 5016 TAACTGATGTTAGCAACATGCTTACAAGAGAGAAAAGCAGCCGTGCATGCCATTGG 5075

Qy 361 TGGAAAGTAAAGTGTACGATGCTGCTTATTAGGAAGCAACAGACGGGTCTGCATGGA 420  
 Db 5076 TGGAAAGTAAAGTGTACGATGCTGCTTATTAGGAAGCAACAGACGGGTCTGCATGGA 5135

Qy 421 TTGGACGAAACCACTAAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 479  
 Db 5136 TTGGACGAAACCACTAAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 5195

Qy 480 ACATTAAGCCATTTGACCATTCACACATTTGGTGGCACCTC 523  
 Db 5196 ACATTAAGCCATTTGACCATTCACACATTTGGTGGCACCTC 5239

RESULT 18

AAT84561  
 ID AAT84561 standard; cDNA; 8591 BP.  
 XX AAT84561;  
 XX 25-MAR-2003 (revised)  
 DT 15-DEC-1997 (first entry)  
 XX Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;  
 KW mutelin; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;  
 KW cyclic.

XX Homo; sapiens.  
 OS Synthetic.  
 OS Chimeric.

PH Key Location/Qualifiers  
 FT CDS 2393..3871  
 FT /\*tag= a

XX U85652092-A.

XX 29-JUL-1997.

XX 05-JUN-1995; 95US-00462859.

XX 01-MAY-1992; 92US-00877675.

XX 20-SEP-1993; 93US-00123659.

XX (AMCY ) AMERICAN CYANAMID CO.  
 XX PA Jacobsen JS, Vitek MP;  
 XX WPI; 1997-392937/36.  
 XX P-FSDS; AAW26393.  
 XX Screening for compounds which reduce beta-amyloid protein formation -  
 PT using cells which express a construct encoding a marker and an amyloid  
 PT precursor muten derived from APP isoforms.  
 XX PS Disclosure; Fig 7; 84pp; English.  
 XX Plasmid pCLL602 (AAW84561), deposited in E. coli as ATCC 69405, codes  
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751  
 CC (see AAW26393), that has a 276-amino acid deletion of the native APP and  
 CC carries Substance P and Met-enkephalin epitope markers placed,  
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid  
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for  
 CC screening for a compound which reduces the formation of beta-amyloid  
 CC protein, determined by measuring the amount of marker in a medium  
 CC containing transfected cells. The method is used to detect compounds  
 CC which inhibit the activity of proteolytic enzymes which cleave APP to  
 CC generate BAP fragments. Such compounds can be used in the treatment of  
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP  
 CC distinguishes the construct from endogenously expressed APP, and  
 CC beneficially increases the resolution of APP-REP fragments resulting from  
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-  
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;  
 XX  
 Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
 Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 Db 4716 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 4775  
 QY 61 ACAAGCAGGCTTGAACGACATATTCGATGAAGAAATCTGCTAGGTTAGCGCTTTGGC 120  
 Db 4776 ACAAGCAGGCTTGAACGACATATTCGATGAAGAAATCTGCTAGGTTAGCGCTTTGGC 4835  
 QY 121 CTGCTTCGCGATGTACGGGCGACATATTCGCGTATCTGAGGGGACTAGCGTGTGTTAGG 180  
 Db 4836 CTGCTTCGCGATGTACGGGCGACATATTCGCGTATCTGAGGGGACTAGCGTGTGTTAGG 4895  
 QY 181 CGAAAAGCGGGCTTTCGGTGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
 Db 4896 CGAAAAGCGGGCTTTCGGTGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 4955  
 QY 241 TTTTGTATAGGAGGGGAAATCTGCTTATGCAATCTCTGTAGTCTTTCGACATCG 300  
 Db 4956 TTTTGTATAGGAGGGGAAATCTGCTTATGCAATCTCTGTAGTCTTTCGACATCG 5015  
 QY 301 TAACGATGATTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCGGATTGG 360  
 Db 5016 TAACGATGATTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCGGATTGG 5075  
 QY 361 TGGAGTAGAGGTGTAAGATCGTGTCTTATTAAGAGGCAACAGACGGGTCTGACATGGA 420  
 Db 5076 TGGAGTAGAGGTGTAAGATCGTGTCTTATTAAGAGGCAACAGACGGGTCTGACATGGA 5135  
 QY 421 TTGAGCAGACCACTAAATTCGGCATTTGCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
 Db 5136 TTGAGCAGACCACTAAATTCGGCATTTGCGAGATAATTGTATTTAAGTGCCTAGCTCGAT 5195  
 QY 480 ACATAAAGCCATTGTACCAATTCACCAATTTGGTGTGACCTC 523  
 Db 5196 ACATAAAGCCATTGTACCAATTCACCAATTTGGTGTGACCTC 5239

RESULT 19  
 AAT87083  
 ID AAT87083 standard; CDNA; 8591 BP.  
 XX AC AAT87083;  
 XX 25-MAR-2003 (revised)  
 DT 06-JAN-1998 (first entry)  
 XX Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.  
 XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;  
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;  
 KW cyclic.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX Key Location/Qualifiers  
 FT CDS 2393..3871  
 FT /\*tag= a  
 FT US5656477-A.  
 XX 12-AUG-1997.  
 XX 20-SEP-1993; 93US-00123659.  
 XX 01-MAY-1992; 92US-00877675.  
 XX (AMCY ) AMERICAN CYANAMID CO.  
 XX Jacobsen JS, Vitek MP;  
 WPI; 1997-414594/38.  
 P-FSDS; AAW26509.  
 Nucleic acid encoding amyloid precursor muten(s) - comprising reporter  
 gene and coding sequence, for identifying compounds which modify the  
 activity of proteolytic enzymes which cleave APP.  
 Disclosure; Fig 7; 84pp; English.  
 Plasmid pCLL602 (AAT87083), deposited in E. coli as ATCC 69405, codes  
 for an amyloid precursor protein (APP) substrate, designated APP-REP 751  
 (see AAW26509), that has a 276-amino acid deletion of the native APP and  
 carries Substance P and Met-enkephalin epitope markers placed,  
 respectively, on the N-terminal and C-terminal sites of the beta-amyloid  
 protein (BAP) domain. APP-REP 751 can be used in a claimed method for  
 screening for a compound which reduces the formation of beta-amyloid  
 protein, determined by measuring the amount of marker in a medium  
 containing transfected cells. The method is used to detect compounds  
 which inhibit the activity of proteolytic enzymes which cleave APP to  
 generate BAP fragments. Such compounds can be used in the treatment of  
 e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP  
 distinguishes the construct from endogenously expressed APP, and  
 beneficially increases the resolution of APP-REP fragments resulting from  
 the proteolytic cleavage by secretase or other amyloidogenic, BAP-  
 generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;  
 SQ  
 Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
 Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 Db 4716 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 4775  
 QY 61 ACAAGCAGGCTTGAACGACATATTCGATGAAGAAATCTGCTAGGTTAGCGCTTTGGC 120





CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-770. These isoforms are derived by alternative splicing. APP-REP 751 is constructed by ligating restriction fragments representing N- and C-terminal APP-751 cDNA and substrate P reporter epitope sequences. APP can be used as a substrate for studying abnormal proteolytic cleavage CC which results in the release of BAP, and also to screen for drugs that CC will inhibit such cleavage

XX SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 60  
DB 4716 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 4775

QY 61 ACAGGCGAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGCG 120  
DB 4776 ACAGGCGAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGCG 4835

QY 121 CTGCTCCGATGTCGCGGACAGATTCGCTATCTAGAGGACGACTAGGTTGTTAGG 180  
DB 4836 CTGCTCCGATGTCGCGGACAGATTCGCTATCTAGAGGACGACTAGGTTGTTAGG 4895

QY 181 CGAAAGCGGGGCTTCGGTTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 240  
DB 4896 CGAAAGCGGGGCTTCGGTTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 4955

QY 241 TTTTGCATAGGAGGGGGAATGAGTCTTATGCAATCTCTTGTAGTCTGCAATGG 300  
DB 4956 TTTTGCATAGGAGGGGGAATGAGTCTTATGCAATCTCTTGTAGTCTGCAATGG 5015

QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360  
DB 5016 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 5075

QY 361 TGGAGTAGGTTGCTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 420  
DB 5076 TGGAGTAGGTTGCTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 5135

QY 421 TTGGACGAACCACTAAATTCGCAATTCGACAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479  
DB 5136 TTGGACGAACCACTAAATTCGCAATTCGACAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 5195

QY 480 ACAATAAGCCCATTTGACCATTCACCAATTTGGTGTGCACCTC 523  
DB 5196 ACAATAAGCCCATTTGACCATTCACCAATTTGGTGTGCACCTC 5239

RESULT 23  
AAV05850 standard; cDNA; 8591 BP.

XX AC AAV05850;  
XX DT 01-JUN-1998 (first entry)  
XX DE APP-REP 751 gene from pCLL621.

XX KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;  
XX epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;  
XX Alzheimer's disease; cleavage; cyclic; circular; ds.  
XX OS Homo sapiens.  
XX Synthetic.  
XX FH Key  
XX FT CDS  
XX PT CDS  
XX /tag= a  
XX /product= "APP-REP\_751"

PN US5693478-A.  
XX 02-DEC-1997.  
XX 05-JUN-1995; 95US-00464247.  
XX 01-MAY-1992; 92US-00877675.  
XX 20-SEP-1993; 93US-00123659.  
XX (AWCY ) AMERICAN CYANAMID CO.  
XX Jacobsen JS, Vitek MP;  
XX WPI; 1998-031744/03.  
XX P-PSDB; AAW44745.  
XX Amyloid precursor mutin reporter molecule assay containing antibody  
XX recognised marker - used to study pathways associated with Alzheimer's  
XX disease.  
XX Disclosure; Fig 8; 84pp; English.

XX This is the nucleotide sequence encoding a novel amyloid precursor  
XX protein (APP) designated APP-REP 751, contained in construct pCLL621. The  
XX sequence encodes a mutant version of the APP 751 isoform of human APP  
XX which contains a deletion of 276 amino acids from the central region. The  
XX deleted region is replaced by a substrate P reporter epitope sequence  
XX (RPRQQFFGLM). In contrast to the APP-REP 751 encoded by the construct  
XX pCLL602 (AAV5849), this sequence does not contain a Met-enkephalin  
XX reporter epitope (YGGPM) fused at the C-terminus of the coding sequence.  
XX The shorter protein is generated for ease of detection based on size  
XX difference with the wild type APP protein and also by detection of the  
XX reporter epitopes. The mutant protein can be used in a method to study  
XX secretase and beta-amyloid protein (BAP)-generating pathways associated  
XX with Alzheimer's disease by studying proteolytic cleavage of the reporter  
XX polypeptides

SQ Sequence 8591 BP; 2225 A; 2038 C; 2248 G; 2080 T; 0 U; 0 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 60  
DB 4716 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 4775

QY 61 ACAGGCGAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGCG 120  
DB 4776 ACAGGCGAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGCG 4835

QY 121 CTGCTCCGATGTCGCGGACAGATTCGCTATCTAGAGGACGACTAGGTTGTTAGG 180  
DB 4836 CTGCTCCGATGTCGCGGACAGATTCGCTATCTAGAGGACGACTAGGTTGTTAGG 4895

QY 181 CGAAAGCGGGGCTTCGGTTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 240  
DB 4896 CGAAAGCGGGGCTTCGGTTGAGGTGCTGAGTAGTGGCGGACGACAAATTTAGCTACA 4955

QY 241 TTTTGCATAGGAGGGGGAATGAGTCTTATGCAATCTCTTGTAGTCTGCAATGG 300  
DB 4956 TTTTGCATAGGAGGGGGAATGAGTCTTATGCAATCTCTTGTAGTCTGCAATGG 5015

QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360  
DB 5016 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 5075

QY 361 TGGAGTAGGTTGCTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 420  
DB 5076 TGGAGTAGGTTGCTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 5135

QY 421 TTGGACGAACCACTAAATTCGCAATTCGACAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479

Db 4716 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGC GCGAGCGAAATTTAAGCTACA 4777



CC e.g. for production of transgenic animals as models for human diseases.  
CC The present sequence is that of a luciferase reporter expression vector,  
CC pRVLuc. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 7223 BP; 1880 A; 1730 C; 1864 G; 1745 T; 0 U; 4 Other;  
Query Match 96.5%; Score 504.6; DB 2; Length 7223;  
Best Local Similarity 99.0%; Pred. No. 1.9e-166;  
Matches 518; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
XX  
SQ 1 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTAGTGGCGGCAAAATTAAGTACA 60  
Dd 2106 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTAGTGGCGGCAAAATTAAGTACA 2165  
Qy 61 ACAAGCAAGGTTGACCGCAATTCGATGAGAAATCTGCTTAGGTTAGCGTTTGG 120  
Dd 2166 ACAAGCAAGGTTGACCGCAATTCGATGAGAAATCTGCTTAGGTTAGCGTTTGG 2225  
Qy 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180  
Dd 2226 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 2285  
Qy 181 CGAAAGCGGGCTTCGCTTGTGACGGGTTAGGATCCCTCAGGATATAGTTCGC 240  
Dd 2286 CGAAAGCGGGCTTCGCTTGTGACGGGTTAGGATCCCTCAGGATATAGTTCGC 2345  
Qy 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Dd 2346 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 2405  
Qy 301 TAAAGATGATTAGCAACATCCCTTACAGGAGAGAAAGACCCGTCGCGATGG 360  
Dd 2406 TAAAGATGATTAGCAACATCCCTTACAGGAGAGAAAGACCCGTCGCGATGG 2465  
Qy 361 TGAAGTAAGTGTACGATCGTCCCTTATAGGAAGGCAACAGACGGTCTGACATGGA 420  
Dd 2466 TGAAGTAAGTGTACGATCGTCCCTTATAGGAAGGCAACAGACGGTCTGACATGGA 2525  
Qy 421 TTGACCAACCACTAATTCGCAATTCGAGAT-ATTGTATTATTAAGTCCCTAGCTCGAT 479  
Dd 2526 TTGACCAACCACTAATTCGCAATTCGAGATATTTTATTAAGTCCCTAGCTCGAT 2585  
Qy 480 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCT 522  
Dd 2586 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCT 2628  
RESULT 26  
ID AAA53869 standard; DNA; 6838 BP.  
XX  
AC AAA53869;  
XX  
DT 03-JAN-2001 (first entry)  
XX  
DE Expression vector pRIG-1.  
XX  
KW Vector; endogenous gene; activation; over-expression; erythropoietin;  
KW growth hormone; drug discovery; granulocyte colony stimulating factor;  
KW ds.  
XX  
OS Synthetic.  
XX  
FN WO200049162-A2.  
XX  
PD 24-AUG-2000.  
XX  
PF 22-FEB-2000; 2000WO-US004429.  
XX  
PR 19-FEB-1999; 99US-00253022.  
PR 08-MAR-1999; 99US-00263814.  
PR 26-MAR-1999; 99US-00276820.  
XX

PA (ATHE-) ATHERSYS INC.  
XX  
PI Harrington UJ, Sherf B, Rundlett S;  
XX  
XX WPI; 2000-549276/50.  
XX  
XX Non-targeted activation of endogenous genes, e.g. for the production of  
XX erythropoietin, growth hormone or granulocyte-colony stimulating factor  
XX proteins and for drug discovery.  
XX  
XX Example 1; Fig 14; 240pp; English.  
XX  
XX New methods, vectors and cells are described for non-targeted activation  
XX and over-expression of endogenous genes. The vector constructs comprise  
XX transcriptional regulatory sequences (TRS) and unpaired splice donor  
XX sequences (USDS), preferably the vectors comprise (in sequential order) a  
XX TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization  
XX site (LS) with a second TRS linked to a selectable marker (SM) lacking a  
XX polyadenylation signal. The methods, vectors and cells comprising the  
XX vectors may be used for the non-targeted activation and over-expression  
XX of endogenous genes, e.g. for the production of proteins (including  
XX erythropoietin, growth hormone or granulocyte-colony stimulating factor)  
XX and drug discovery. The advantage of these methods are that endogenous  
XX genes including those associated with human disease and development, may  
XX be activated and isolated without prior knowledge of the sequence  
XX structure, function or expression profile of the genes being known  
XX  
SQ Sequence 6838 BP; 1679 A; 1669 C; 1709 G; 1781 T; 0 U; 0 Other;  
Query Match 95.8%; Score 500.8; DB 3; Length 6838;  
Best Local Similarity 98.5%; Pred. No. 4.1e-165;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGGCAAAATTTAAGTACA 60  
Dd 1300 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGGCAAAATTTAAGTACA 1359  
Qy 61 ACAAGCAAGGTTGACCGCAATTCGATGAGAAATCTGCTTAGGTTAGCGTTTGG 120  
Dd 1360 ACAAGCAAGGTTGACCGCAATTCGATGAGAAATCTGCTTAGGTTAGCGTTTGG 1419  
Qy 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180  
Dd 1420 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 1479  
Qy 181 CGAAAGCGGGCTTCGCTTGTGACGGGTTAGGATCCCTCAGGATATAGTTCGC 240  
Dd 1480 CGCCCAAGCGGGCTTCGCTTGTGACGGGTTAGGATCCCTCAGGATATAGTTCGC 1539  
Qy 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Dd 1540 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1599  
Qy 301 TAAAGTAAGTGTACCAATTCGCTTACAGGAGAGAAAGACCCGTCGCGATGG 360  
Dd 1600 TAAAGTAAGTGTACCAATTCGCTTACAGGAGAGAAAGACCCGTCGCGATGG 1659  
Qy 361 TGAAGTAAGTGTACCAATTCGCTTACAGGAGAGAAAGACCCGTCGCGATGG 420  
Dd 1660 TGAAGTAAGTGTACCAATTCGCTTACAGGAGAGAAAGACCCGTCGCGATGG 1719  
Qy 421 TTGACCAACCACTAATTCGCAATTCGAGAT-ATTGTATTATTAAGTCCCTAGCTCGAT 479  
Dd 1720 TTGACCAACCACTAATTCGCAATTCGAGATATTTTATTAAGTCCCTAGCTCGAT 1779  
Qy 480 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Dd 1780 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1823  
RESULT 27  
ID ABL57333 standard; DNA; 8902 BP.  
XX

QY	121	CTGCTTCGCGATGTACGGGCCAGATATTCCGCTATCTGAGTATCTGAGGGGACTAGGGGTGTGTTAGG	3544
Db	3485	CTGCTTCGCGATGTACGGGCCAGATATACGCGTATCTGAGGGGACTAGGGGTGTGTTAGG	3544
QY	181	CGAAGAGCGGGGCTTCGGTCTGACGGGTTAGGAGTCCCTCTCAGCATATAGTAGTTTCGC	240
Db	3545	CGCCCGAGCGGGGCTTCGGTCTGACGGGTTAGGAGTCCCTCTCAGCATATAGTAGTTTCGC	3604
QY	241	TTTTTCATATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTTGCAACATGG	300
Db	3605	TTTTTCATATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTTGCAACATGG	3664
QY	301	TAACTAGTGTAGCAACATGCTTACAGGAGAGAAAGCAACGCTGCATGCCGATGG	360
Db	3665	TAACTAGTGTAGCAACATGCTTACAGGAGAGAAAGCAACGCTGCATGCCGATGG	3724
QY	361	TGGAAGTAAAGTGTACGATGTCGCTTATATAGGAAGCAACAGACGGGTCTGCACATGGA	420
Db	3725	TGGAAGTAAAGTGTACGATGTCGCTTATATAGGAAGCAACAGACGGGTCTGCACATGGA	3784
QY	421	TTGGACGAACCACTAAATTCGCAATGCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT	479
Db	3785	TTGGACGAACCACTAAATTCGCAATGCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT	3844
QY	480	ACATATAACGCGATTTTGACCAATTCACCAATTTGGTGTGCACCTC	523
Db	3845	ACATATAACGCGATTTTGACCAATTCACCAATTTGGTGTGCACCTC	3888
RESULT 28			
AA453873			
ID	AA453873 standard; DNA; 9725 BP.		
AC	AA453873;		
DT	03-JAN-2001 (first entry)		
DE	Expression vector pRIG19.		
XX	Vector; endogenous gene; activation; over-expression; erythropoietin; growth hormone; drug discovery; granulocyte colony stimulating factor; ds.		
XX	Synthetic.		
XX	W0200049162-A2.		
XX	24-AUG-2000.		
XX	22-FEB-2000; 2000WO-US004429.		
XX	19-FEB-1999; 99US-00253022.		
XX	08-MAR-1999; 99US-00263814.		
XX	26-MAR-1999; 99US-00276820.		
XX	(ATHE-) ATHERSYS INC.		
XX	Harrington JJ, Sherf B, Rundlett S;		
XX	WPI; 2000-549276/50.		
XX	Non-targeted activation of endogenous genes, e.g. for the production of erythropoietin, growth hormone or granulocyte-colony stimulating factor proteins and for drug discovery.		
XX	Disclosure; Fig 30; 240pp; English.		
XX	New methods, vectors and cells are described for non-targeted activation and over-expression of endogenous genes. The vector constructs comprise transcriptional regulatory sequences (TRS) and unpaired splice donor sequences (USDS), preferably the vectors comprise (in sequential order) a TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization site (LS) with a second TRS linked to a selectable marker (SW) lacking a		

CC polyadenylation signal. The methods, vectors and cells comprising the  
 CC vectors may be used for the non-targeted activation and over-expression  
 CC of endogenous genes, e.g. for the production of proteins (including  
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)  
 CC and drug discovery. The advantage of these methods are that endogenous  
 CC genes including those associated with human disease and development, may  
 CC be activated and isolated without prior knowledge of the sequence  
 CC structure, function or expression profile of the genes being known  
 XX  
 SQ Sequence 9725 BP; 2425 A; 2507 C; 2448 G; 2343 T; 0 U; 2 Other;  
 Query Match 95.8%; Score 500.8; DB 3; Length 9725;  
 Best Local Similarity 98.5%; Pred. No. 4.9e-165;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 XX  
 QY 1 CTGCTCCCTGCTGTGTGTGGAGTCTGCTAGTGTGCGGAGGCAAAATTAAGCTACA 60  
 DB 1149 CTGCTCCCTGCTGTGTGTGGAGTCTGCTAGTGTGCGGAGGCAAAATTAAGCTACA 1208  
 QY 61 ACAGGCAAGGCTTACCGACAAATTCATGATGAGTCTGTAGGCTTAGCGTTTGG 120  
 DB 1209 ACAGGCAAGGCTTACCGACAAATTCATGATGAGTCTGTAGGCTTAGCGTTTGG 1268  
 QY 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTT 180  
 DB 1269 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTT 1328  
 QY 181 CGAAAGCGGGGCTTCGCTTACCGGCTTACGGGCTTACGGGCTTACGGGCTTAC 240  
 DB 1329 CGCCCGAGCGGGCTTCGCTTACCGGCTTACGGGCTTACGGGCTTACGGGCTT 1388  
 QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
 DB 1389 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1448  
 QY 301 TAACCATGAGTGTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 360  
 DB 1449 TAACCATGAGTGTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 1508  
 QY 361 TGAAGTAAGTGTACGATGCTGCTTATAGGAGGACACAGCGGTCTGACATGGA 420  
 DB 1509 TGAAGTAAGTGTACGATGCTGCTTATAGGAGGACACAGCGGTCTGACATGGA 1568  
 QY 421 TTGACGACGACATTAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 479  
 DB 1569 TTGACGACGACATTAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 1628  
 QY 480 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGTGACCTC 523  
 DB 1629 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGTGACCTC 1672  
 RESULT 29  
 AAAS3879  
 ID AAAS3879 standard; DNA; 9732 BP.  
 XX  
 AC AAAS3879;  
 XX  
 DT 03-JAN-2001 (first entry)  
 XX  
 DE Expression vector pRIG-TP.  
 XX  
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;  
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;  
 KW ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200049162-A2.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 22-FEB-2000; 2000WO-US004429.

XX 19-FEB-1999; 99US-00253022.  
 PR 08-VAR-1999; 99US-00263814.  
 PR 26-MAR-1999; 99US-00276820.  
 XX  
 FA (ATHE-) ATHERSYS INC.  
 XX  
 PI Harrington JJ, Sherf B, Rundlett S;  
 XX  
 XX WPI; 2000-549276/50.  
 XX  
 PT Non-targeted activation of endogenous genes, e.g. for the production of  
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor  
 PT proteins and for drug discovery.  
 XX  
 PS Example 15; Fig 37; 240pp; English.  
 CC  
 CC New methods, vectors and cells are described for non-targeted activation  
 CC and over-expression of endogenous genes. The vector constructs comprise  
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor  
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a  
 CC TRS, an USDS, a rare cutting restriction site (RCS) and a linearization  
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a  
 CC polyadenylation signal. The methods, vectors and cells comprising the  
 CC vectors may be used for the non-targeted activation and over-expression  
 CC of endogenous genes, e.g. for the production of proteins (including  
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)  
 CC and drug discovery. The advantage of these methods are that endogenous  
 CC genes including those associated with human disease and development, may  
 CC be activated and isolated without prior knowledge of the sequence  
 CC structure, function or expression profile of the genes being known  
 XX  
 SQ Sequence 9732 BP; 2427 A; 2512 C; 2443 G; 2348 T; 0 U; 2 Other;  
 Query Match 95.8%; Score 500.8; DB 3; Length 9732;  
 Best Local Similarity 98.5%; Pred. No. 4.9e-165;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTGGAGTCTGCTAGTGTGCGGAGGCAAAATTAAGCTACA 60  
 DB 1152 CTGCTCCCTGCTGTGTGTGGAGTCTGCTAGTGTGCGGAGGCAAAATTAAGCTACA 1211  
 QY 61 ACAGGCAAGGCTTACCGACAAATTCATGATGAGTCTGTAGGCTTAGCGTTTGG 120  
 DB 1212 ACAGGCAAGGCTTACCGACAAATTCATGATGAGTCTGTAGGCTTAGCGTTTGG 1271  
 QY 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTT 180  
 DB 1272 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTT 1331  
 QY 181 CGAAAGCGGGGCTTCGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTAC 240  
 DB 1332 CGCCCGAGCGGGCTTCGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTAC 1391  
 QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
 DB 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1451  
 QY 301 TAACCATGAGTGTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 360  
 DB 1452 TAACCATGAGTGTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATGG 1511  
 QY 361 TGAAGTAAGTGTACGATGCTGCTTATAGGAGGACACAGCGGTCTGACATGGA 420  
 DB 1512 TGAAGTAAGTGTACGATGCTGCTTATAGGAGGACACAGCGGTCTGACATGGA 1571  
 QY 421 TTGACGACGACATTAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 479  
 DB 1572 TTGACGACGACATTAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 1631  
 QY 480 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGTGACCTC 523  
 DB 1632 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGTGACCTC 1675

QY	181	CGAAAAACGGGGCTTCGGTGTACGGGGTTAGGAGTCCCTCAGCATATAGTAGTTTCGC	240
Db	1471	CGCCACAGCGGGCTTCGGTGTACGGGGTTAGGAGTCCCTCAGCATATAGTAGTTTCGC	1530
QY	241	TTTTTCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTTGATCTTGCACATGG	300
Db	1531	TTTTTCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTTGATCTTGCACATGG	1590
QY	301	TAAAGATAGTTAGCAACATGCTTACIAGGAGAGAAAAGCACCGTCGATGCCGATTGG	360
Db	1591	TAAAGATAGTTAGCAACATGCTTACIAGGAGAGAAAAGCACCGTCGATGCCGATTGG	1650
QY	361	TGGAAGTAAGGTGGTACGATCGTGCCTTATTAGGAAGGCACAGACGGGTCTGACATGGA	420
Db	1651	TGGAAGTAAGGTGGTACGATCGTGCCTTATTAGGAAGGCACAGACGGGTCTGACATGGA	1710
QY	421	TTGGAAGCAACCTAAATTCGGCATTTGCAGAGAT-ATTGTATTAACTGCTAGCTCCGAT	479
Db	1711	TTGGAAGCAACCTAAATTCGGCATTTGCAGAGAT-ATTGTATTAACTGCTAGCTCCGAT	1770
QY	480	ACATATAACCCATTGTACCACTTACCACATTTGGTGTGCACCTC	523
Db	1771	ACATATAACCCATTGTACCACTTACCACATTTGGTGTGCACCTC	1814
RESULT 31			
ID	AAV59501 standard; DNA; 11265 BP.		
XX	AAV59501;		
AC	AAV59501;		
XX	17-OCT-2003 (revised)		
DT	02-FEB-1999 (first entry)		
DT	XX		
DE	Plasmid pREP7::CTL44-hlg.		
XX	XX		
XX	pREP7::CTL44-hlg; plasmid; CTL44; immunoglobulin; vaccine;		
KW	DNA immunisation; human; mouse; ds; circular; cyclic.		
OS	Homo sapiens.		
OS	Mus sp.		
OS	Chimeric.		
XX	XX		
PN	W09844129-A1.		
PD	08-OCT-1998.		
XX	XX		
PF	26-MAR-1998; 98WO-AU00208.		
XX	XX		
PR	27-MAR-1997; 97AU-00005891.		
PR	13-FEB-1998; 98AU-00001830.		
XX	XX		
PA	{COIN-} COUNCIL QUEENSLAND INST MEDICAL RES.		
PA	{CSR-} COMMONWEALTH SCI & IND RES ORG.		
PA	{UYME-} UNIV MELBOURNE.		
PA	{HALL-} HALL INST MEDICAL RES WALTER & ELIZA.		
PA	{CSLC-} CSL LTD.		
XX	XX		
PI	Boyle JS, Brady JL, Lew AM;		
XX	XX		
DE	WPI; 1998-557122/47.		
XX	XX		
PT	DNA molecule for raising an immune response to antigen - comprises		
PT	sequence encoding dimerisation or multimerisation polypeptide.		
XX	XX		
PS	Disclosure; Page 32-37; 64pp; English.		
XX	XX		
CC	This is the DNA sequence of expression plasmid pREP7::CTL44-hlg that		
CC	encodes a secreted form of the Fc fragment of human IgG1 fused to murine		
CC	CTL44. The invention provides a new DNA molecule for use in raising an		
CC	immune response to an antigen. The DNA molecule comprises: (i) a first		
CC	sequence encoding a targeting molecule (e.g. CTL44, which acts as a		
CC	targeting molecule to antigen-presenting cells expressing B-7); (ii) a		



QY  
121 CTGCTTCGGCATGTACGGCCAGATAATTCGGGTATCTGAGGGACTAGGGTG'GT'TAGG TBU

XX

59077

RESULT 36  
AAA59077







CC protein or its portion, and selectively transduces photoreceptors and  
CC delivers a gene product encoded by AAV. The present sequence represents  
CC the nucleotide sequence of plasmid MMTV-E2a-SV40-Neo  
XX  
SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;  
Query Match 82.4%; Score 430.8; DB 6; Length 11600;  
Best Local Similarity 99.5%; Pred. No. 2.6e-140; Indels 0; Gaps 0;  
Matches 432; Conservative 0; Mismatches 2;  
QY 1 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAAGCTACA 60  
Db 11167 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAAGCTACA 11226  
QY 61 ACAAGCCAAAGGCTTGACCGCAATTCGATGAAGAACTCTGCTTAGGGTTAGCGTTTGGC 120  
Db 11227 ACAAGCCAAAGGCTTGACCGCAATTCGATGAAGAACTCTGCTTAGGGTTAGCGTTTGGC 11286  
QY 121 CTGCTTCGCGATGTACGGCCAGATATTCGGTATCTGAGGGCACTAGGGTGTGTTAGG 180  
Db 11287 CTGCTTCGCGATGTACGGCCAGATATTCGGTATCTGAGGGCACTAGGGTGTGTTAGG 11346  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGC 240  
Db 11347 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGC 11406  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 11466  
QY 301 TAAAGTGTAGTGTACGACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 360  
Db 11467 TAAAGTGTAGTGTACGACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 11526  
QY 361 TGGAGTAAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 11586  
Db 11527 TGGAGTAAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 11586  
QY 421 TTGGACGACCACT 434  
Db 11587 TTGGACGACCACT 11600  
RESULT 38  
AAL56865  
ID AAL56865 standard; DNA; 11600 BP.  
AC AAL56865;  
XX  
DT 06-NOV-2003 (first entry)  
DE DNA sequence of the plasmid MMTV-E2a-SV40-Neo construct.  
XX  
KW Fibre shaft modification; adenoviral vector; cell entry pathway; penton;  
KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;  
KW gene therapy; fibre knob; ds.  
XX  
OS Rhesus macaque polyoma virus.  
OS Unidentified adenovirus.  
OS Unidentified.  
XX  
PN WO2003062400-A2.  
XX  
PD 31-JUL-2003.  
XX  
PF 24-JAN-2003; 2003WO-US002295.  
XX  
PR 24-JAN-2002; 2002US-0350388P.  
PR 26-JUN-2002; 2002US-0331967P.  
XX  
PA (SCRI) SCRIPPS RES INST.  
PA (NOVS) NOVARTIS AG.  
XX

PI Kalexo M, Nemerow GR, Smith T, Stevenson SC;  
XX  
DR WPI; 2003-627459/59.  
XX  
PT New modified adenovirus capsid protein, useful as a base vector for  
PT producing redirected adenoviruses.  
XX  
PS Disclosure; Page 143-146; 132pp; English.  
XX  
CC This invention relates to novel fibre shaft modifications in adenoviral  
CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a  
CC specific targeted tissue or organ, accordingly gene therapy requires the  
CC ablation of normal virus tropism. If successful, systemic vector delivery  
CC into a peripheral vein would be targeted to the desired location in the  
CC body without any associated side effects, which would permit lower, less  
CC toxic vector doses that are also potentially less immunogenic. The  
CC present invention describes capsid modifications, specifically fibre  
CC shaft mutations that when expressed on adenoviral particles ablated  
CC binding to heparin sulphate proteoglycans (HSP) thus providing detached  
CC vectors. Furthermore, when this is combined with modifications of other  
CC adenoviral proteins involved in the cell entry pathway such as the fibre  
CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors  
CC become fully detargeted. As such, these fully ablated particles can be  
CC used in vivo as base vectors for producing redirected adenoviruses with  
CC the desired cell specificity. This polynucleotide sequence is the plasmid  
CC MMTV-E2a-SV40-Neo construct used to provide complementation of the  
CC adenoviral E2a function of the invention  
XX  
SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;  
Query Match 82.4%; Score 430.8; DB 8; Length 11600;  
Best Local Similarity 99.5%; Pred. No. 2.6e-140; Indels 0; Gaps 0;  
Matches 432; Conservative 0; Mismatches 2;  
QY 1 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAAGCTACA 60  
Db 11167 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAAGCTACA 11226  
QY 61 ACAAGCCAAAGGCTTGACCGCAATTCGATGAAGAACTCTGCTTAGGGTTAGGGTTTGGC 120  
Db 11227 ACAAGCCAAAGGCTTGACCGCAATTCGATGAAGAACTCTGCTTAGGGTTAGGGTTTGGC 11286  
QY 121 CTGCTTCGCGATGTACGGCCAGATATTCGGTATCTGAGGGCACTAGGGTGTGTTAGG 180  
Db 11287 CTGCTTCGCGATGTACGGCCAGATATTCGGTATCTGAGGGCACTAGGGTGTGTTAGG 11346  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGC 240  
Db 11347 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGC 11406  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 11466  
QY 301 TAAAGTGTAGTGTACGACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 360  
Db 11467 TAAAGTGTAGTGTACGACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 11526  
QY 361 TGGAGTAAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 420  
Db 11527 TGGAGTAAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 11586  
QY 421 TTGGACGACCACT 434  
Db 11587 TTGGACGACCACT 11600  
RESULT 39  
AD575125  
ID AD575125 standard; DNA; 11600 BP.  
XX  
AC ADB75125;  
XX

DT 04-DEC-2003 (first entry)  
 XX Chromosomal insertion pMNeOE2a-3.1.  
 DE  
 XX ophthalmological; antiinflammatory; antidiabetic; gene therapy;  
 KW adenovirus inverted terminal repeat sequence;  
 KW adenovirus packaging signal; photoreceptor-specific promoter;  
 KW adenovirus type 3; adenovirus type D serotype; adenovirus type 2;  
 KW adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor;  
 KW rhodopsin; wild-type Stargardt disease gene; STGD1; anti-cancer agent;  
 KW retinal degenerative disease; retinitis pigmentosa; Stargardt's disease;  
 KW diabetic retinopathy; retinal vascularisation; choroidaemia;  
 KW gyrate atrophy; macular dystrophy; retinoblastoma;  
 KW photoreceptor-restricted transgene expression;  
 KW recombinant adenovirus vector; adenovirus type 5; E2a;  
 KW chromosomal insertion; ds.  
 XX Homo sapiens.  
 OS  
 XX US2002193327-A1.  
 PN  
 XX 19-DEC-2002.  
 PD  
 XX  
 XX 01-MAY-2001; 2001US-00847101.  
 PF  
 XX  
 XX 01-MAY-2000; 2000US-00562934.  
 PR  
 XX (Scri ) SCRIPPS RES INST.  
 PA  
 XX  
 XX Nemrow GR, Von Seggern DJ, Friedlander M;  
 FI  
 XX WPI; 2003-657234/62.  
 DR  
 XX Novel nucleic acids comprising adenovirus inverted terminal repeat  
 PT sequences, adenovirus packaging signals operatively linked to the  
 PT sequences and photoreceptor-specific promoters, useful for treating  
 PT retinitis pigmentosa.  
 PT  
 XX Example 5; Page 93-98; 106pp; English.  
 PS  
 XX The invention describes an isolated nucleic acid (I) comprising  
 CC adenovirus inverted terminal repeat sequence, and an adenovirus packaging  
 CC signal operatively linked to the sequence, and a photoreceptor-specific  
 CC promoter. A recombinant adenovirus vector (II) comprising (I) is useful  
 CC for targeted delivery of a gene product to the eye of a mammal which  
 CC involves administering (II) that comprises heterologous DNA encoding the  
 CC gene product or resulting in expression of the gene product, where the  
 CC recombinant virus comprises a fibre protein that specifically or  
 CC selectively binds to receptors that are expressed on cells which are  
 CC photoreceptors, in the eye. The recombinant virus comprises a fibre  
 CC protein which is an adenovirus type 37, from an adenovirus type D  
 CC serotype. The fibre is a chimeric protein containing a sufficient portion  
 CC of the N-terminus of an adenovirus type 2 or type 5 fibre protein for  
 CC interaction with an adenovirus type 2 or type 5 penton, and a sufficient  
 CC portion of an adenovirus serotype D knob portion of the fibre for  
 CC selective binding to photoreceptors in the eye of a mammal. The  
 CC encapsulated nucleic acid comprises a photoreceptor-specific promoter  
 CC operatively linked to a nucleic acid comprising the therapeutic product  
 CC which is chosen from trophic factor, anti-apoptotic factor, gene encoding  
 CC a rhodopsin protein, wild-type Stargardt disease gene (STGD1), an anti-  
 CC cancer agent and a protein that regulates expression of a photoreceptor-  
 CC specific gene product. The delivery is effected for treatment of an  
 CC ocular disease such as retinal degenerative disease e.g., retinitis  
 CC pigmentosa, Stargardt's disease, diabetic retinopathies, retinal  
 CC vascularisation, choroidaemia, gyrate atrophy or macular dystrophy or  
 CC retinoblastoma inherited and acquired retinal and neovascular  
 CC degenerative diseases. The viral nucleic acid comprises an adenovirus  
 CC inverted terminal repeat (ITR) sequences, and an adenovirus packaging  
 CC signal operatively linked to the sequence. The ITRs and packaging signal  
 CC are derived from an adenovirus serotype B or C, or adenovirus type 2 or  
 CC 5. The viral nucleic acid further comprises a photoreceptor-specific  
 CC promoter. (II) includes photoreceptor promoters providing a means not  
 CC only for specific targeting of expression in these cells, but also for

CC photoreceptor-restricted transgene expression. This sequence represents a  
 CC chromosomal insertion found in adenoviral plasmids of the A519 lung  
 CC carcinoma cell line which provide a complement of adenoviral E2a gene  
 CC function.  
 XX  
 XX Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;  
 Query Match 82.4%; Score 430.8; DB 9; Length 11600;  
 Best Local Similarity 99.5%; Fred. No. 2.6e-140;  
 Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 CTGCTCCCTGCTTGCTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTTACA 60  
 Db 11167 CTGCTCCCTGCTTGCTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTTACA 11226  
 QY 61 ACAAGGCAAGGCTTACCGACAATTCATGAAGAATCTGCTTAGGGTTAGCGCTTTGGCG 120  
 Db 11227 ACAAGGCAAGGCTTACCGACAATTCATGAAGAATCTGCTTAGGGTTAGCGCTTTGGCG 11286  
 QY 121 CTGCTTCGGATCTACGGGCGCATATTCGGTATCTCGAGGGGACTAGGGTGTGTTAGG 180  
 Db 11347 CGAAGAGCGGGGCTTCGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 11406  
 QY 241 TTTTGCATAGGAGGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db 11407 TTTTGCATAGGAGGGGGGAATGTAGTCTTATGCAATCACTTGTAGTCTTGCACATGG 11466  
 QY 301 TACGATGATTTAGCAACATGCTTACAGGAGAGAAAAGCACCCTGCATGCCGATTGG 360  
 Db 11467 TACGATGATTTAGCAACATGCTTACAGGAGAGAAAAGCACCCTGCATGCCGATTGG 11526  
 QY 361 TCGAAGTAAGTGTGATACGATCGTCTCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
 Db 11527 TCGAAGTAAGTGTGATACGATCGTCTCTTATTAGGAGGCAACAGACGGTCTGCATGGA 11586  
 QY 421 TTGGACGACCACT 434  
 Db 11587 TTGGACGACCACT 11600  
 RESULT 40  
 AAA14722  
 ID AAA14722 standard; DNA; 2187 BP.  
 AC AAA14722;  
 XX  
 XX 06-AUG-2003 (revised)  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Nucleotide sequence of region A of vector AdRSVbeta-lactamase.  
 XX Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;  
 KW replication-deficient adenovirus type 5; suicide gene therapy;  
 KW cancer cell; chemotherapy; beta-lactamase producing enzyme; produg TCM;  
 KW anticancer; tumor; leukemia; breast cancer; Wilms tumor;  
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;  
 KW papillary adenocarcinoma; es.  
 XX  
 OS Synthetic.  
 OS Rous sarcoma virus.  
 OS Mastadenovirus.  
 XX WO2000020608-A1.  
 PN  
 XX 13-APR-2000.  
 PD  
 XX 01-OCT-1999; 99WO-US020908.  
 PF  
 XX 02-OCT-1998; 98US-00165321.  
 PR

XX (GENO-) GENOTHERAPEUTICS INC.  
 XX Steiner MS;  
 XX WPI; 2000-303788/26.  
 XX  
 XX Treating cancer using viral vectors which encode enzymes that convert  
 XX inactive drugs to active cytotoxic agents, expression of the enzyme is  
 XX tissue specific therefore targeting the effects of the drug to tumor  
 XX cells.  
 XX  
 XX Disclosure; Fig 10; 130pp; English.  
 XX  
 XX The specification describes a method for inducing cellular cytotoxicity  
 XX in tumor cells using replication-deficient adenovirus type 5 expression  
 XX vectors. The vectors comprise a sequence encoding a beta-lactamase under  
 XX the control of a Rous Sarcoma virus in combination with a prodrug  
 XX conjugated to a toxic agent. Tissue specific expression of the enzyme  
 XX converts the inactive drugs into active cancer killing agents. The  
 XX adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-  
 XX lactamase sequence is inserted within this region. The vectors are used  
 XX for suicide gene therapy. This involves introducing genes into cancer  
 XX cells that encode enzymes capable of converting inactive drugs into  
 XX active cancer killing agents. If tissue specific promoters are coupled to  
 XX the prodrug enzymes, then production of the prodrug will be tissue  
 XX specific and targeted to the tumor. Therefore the cancer cells act as  
 XX their own factories to activate chemotherapy agents and commit suicide.  
 XX Beta-lactamase prodrug enzymes convert prodrug TCM into an active  
 XX anticancer agent which is cytotoxic to cancer cells PFC-1. The method is  
 XX used to treat patients with cancers of the brain, bladder or prostate. It  
 XX may also be used to treat a range of other tumors such as leukemia,  
 XX breast cancer, Wilms' tumor, small cell lung carcinoma, Ewing's sarcoma,  
 XX colon carcinoma and papillary adenocarcinomas. The present sequence  
 XX represents region A of vector AdRSVbeta-lactamase, a vector of the  
 XX invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 XX Sequence 2187 BP; 562 A; 477 C; 592 G; 556 T; 0 U; 0 Other;  
 XX  
 XX Query Match 75.1%; Score 393; DB 3; Length 2187;  
 XX Best Local Similarity 98.8%; Pred. No. 2.4e-127;  
 XX Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 QY 123 GTTTCGGATGTACGGCGCCAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGCGG 182  
 Db 404 GCGCCCGATGTACGGCGCCAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGCGG 463  
 QY 183 AAAAGCGGGCTTCGGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATTCGCTT 242  
 Db 464 AAAAGCGGGCTTCGGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATTCGCTT 523  
 QY 243 TTGCATAGGAGGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGGTA 302  
 Db 524 TTGCATAGGAGGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGGTA 583  
 QY 303 ACGATAGTGTAGCAATGCTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362  
 Db 584 ACGATAGTGTAGCAATGCTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643  
 QY 363 GAACTAGGTGTAGCAATGCTTTATAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 422  
 Db 644 GAACTAGGTGTAGCAATGCTTTATAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 703  
 QY 423 GGACGAACCACTAAATTCGGCATTTGCAGATATTTGATTTAAGTCCCTAGTCCGATACA 482  
 Db 704 GGACGAACCACTAAATTCGGCATTTGCAGATATTTGATTTAAGTCCCTAGTCCGATACA 763  
 QY 483 ATAAAGCCCAATTTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCA 523  
 Db 764 ATAAAGCCCAATTTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCA 804

AAZ93333  
 ID AAZ93333 standard; DNA; 2829 BP.  
 XX  
 XX AAZ93333;  
 XX  
 XX 04-JUL-2000 (first entry)  
 XX  
 XX Partial sequence of replication deficient adenoviral vector AdRSV2C9.  
 XX  
 XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 XX prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200014256-A1.  
 XX  
 XX 16-MAR-2000.  
 XX  
 XX 03-SEP-1999; 99WO-US018834.  
 XX  
 XX 04-SEP-1998; 98US-00148275.  
 XX  
 XX (GENO-) GENOTHERAPEUTICS INC.  
 XX  
 XX Steiner MS, Lu Y;  
 XX  
 XX WPI; 2000-257001/22.  
 XX  
 XX Replication-deficient adenovirus type 5 expression vectors used for gene  
 XX therapy of cancer, especially prostate cancer, comprising an insertion of  
 XX nucleic acid encoding cytochrome p450 genes.  
 XX  
 XX Claim 16; Fig 11A; 110pp; English.  
 XX  
 XX Replication-deficient adenovirus type 5 expression vectors comprise an  
 XX adenovirus genome with a deletion in the E1 and E2 region of the genome  
 XX and an insertion within the region under the control of a Rous Sarcoma  
 XX virus promoter can be used to induce chemotoxicity in tumour cells. Three  
 XX such expression vectors are described, the inserted nucleic acids in each  
 XX being the following: Vector (I) has an insertion of a nucleic acid  
 XX encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-  
 XX 2628). Vector (II) has an insertion of a nucleic acid encoding a  
 XX cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector  
 XX (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 XX dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 XX designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell  
 XX can be induced by administering (I) and (III) or (II) and (III) into the  
 XX tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell  
 XX to a prodrug and then administering the prodrug which kills the cell,  
 XX inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 XX therapy to transfer a drug susceptibility gene to the tumor which can kill  
 XX activates a nontoxic prodrug intratumorally so the released drug can kill  
 XX the tumor cells containing the drug susceptibility gene. This sequence is  
 XX designated region A of the vector AdRSV2C9 and is the sequence of the  
 XX cytochrome 2C9 p450  
 XX  
 XX Sequence 2829 BP; 748 A; 633 C; 707 G; 741 T; 0 U; 0 Other;  
 XX  
 XX Query Match 75.1%; Score 393; DB 3; Length 2829;  
 XX Best Local Similarity 98.8%; Pred. No. 2.7e-127;  
 XX Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 QY 123 GTTTCGGATGTACGGCGCCAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGCGG 182  
 Db 404 GCGCCCGATGTACGGCGCCAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGCGG 463  
 QY 183 AAAAGCGGGCTTCGGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATTCGCTT 242  
 Db 464 AAAAGCGGGCTTCGGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATTCGCTT 523  
 QY 243 TTGCATAGGAGGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGGTA 302

Db 524 TTGCATAGGGAGGGGAATGTAGTCTTATGCAATACCTTGTAGTCTGCAACATGGTA 583  
 Qy 303 ACGATGATTAGCAACATGCTTACAGAGAGAGAAAGACCGTGTGATGCCGATGGTG 362  
 Db 584 ACGATGATTAGCAACATGCTTACAGAGAGAGAAAGACCGTGTGATGCCGATGGTG 643  
 Qy 363 GAGTAAGGTGATGACGATGCTGCTTATAGGAAGGCAACAGACGGTCTGACATGGATT 422  
 Db 644 GAGTAAGGTGATGACGATGCTGCTTATAGGAAGGCAACAGACGGTCTGACATGGATT 703  
 Qy 423 GGACGAACCACTAAATTCGCGATTGACAGAGATATTGATTTAAGTGGCTAGCTCGATACA 482  
 Db 704 GGACGAACCACTGATTCGCGATTGACAGAGATATTGATTTAAGTGGCTAGCTCGATACA 763  
 Qy 483 ATAAACGCCATTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCAATTC 523  
 Db 764 ATAAACGCCATTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCAATTC 804

RESULT 42  
 AAZ93078  
 ID AAZ93078 standard; DNA; 2878 BP.  
 XX  
 AC AAZ93078;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 DE Partial sequence of replication deficient adenoviral vector Ad5RSV3A4.  
 XX  
 KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200014256-A1.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 03-SEP-1999; 99WO-US018834.  
 XX  
 PR 04-SEP-1998; 98US-00148275.  
 XX  
 PA (GENO-) GENOTHERAPEUTICS INC.  
 XX  
 PI Steiner MS, Lu Y;  
 XX  
 DR WPI; 2000-257001/22.  
 XX

PT Replication-deficient adenovirus type 5 expression vectors used for gene  
 therapy of cancer, especially prostate cancer, comprising an insertion of  
 PT nucleic acid encoding cytochrome p450 genes.  
 XX

PS Claim 17; Fig 11B; 110pp; English.  
 XX  
 CC Replication-deficient adenovirus type 5 expression vectors comprise an  
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome  
 CC and an insertion within the region under the control of a Rous Sarcoma  
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three  
 CC such expression vectors are described, the inserted nucleic acids in each  
 CC being the following: Vector (I) has an insertion of a nucleic acid  
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV209 (ATCC VR-  
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a  
 CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector  
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 CC designated Ad5RSVRD (ATCC VR-2630). The chemotoxicity of a tumor cell  
 CC can be induced by administering (I) and (III) or (II) and (III) into the  
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell  
 CC to a prodrug and then administering the prodrug which kills the cell,  
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 CC therapy to transfer a drug susceptibility gene to the tumor which  
 CC activates a nontoxic prodrug intratumorally so the released drug can kill

CC the tumor cells containing the drug susceptibility gene. This sequence is  
 CC designated region A of the vector Ad5RSV3A4 and is the sequence of the  
 CC cytochrome 3A4 p450

SQ Sequence 2878 BP; 786 A; 609 C; 710 G; 773 T; 0 U; 0 Other;  
 Query Match 75.1%; Score 393; DB 3; Length 2878;  
 Best Local Similarity 98.8%; Pred. No. 2.7e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 123 GCTTCGCGATTGACGGCGAGATATTCGCGATTGACGGCGAGTGGTGTGTTAGGCG 182  
 Db 404 GCGCCCGGATGTGACGGCGAGATATACGCGTATCTGAGGGGACTAGGGGTGTGTTAGGCG 463  
 Qy 183 AAAAGCGGGGCTTCGGTTGTAGCGGTTAGCGGTTAGCGGTTAGCGGTTAGCGGTTAGCGGTT 242  
 Db 464 AAAAGCGGGGCTTCGGTTGTAGCGGTTAGCGGTTAGCGGTTAGCGGTTAGCGGTTAGCGGTT 523  
 Qy 243 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAATGGTA 302  
 Db 524 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAATGGTA 583  
 Qy 303 ACGATGATTAGCAACATGCTTACAGAGAGAGAAAGACCGTGTGATGCCGATGGTG 362  
 Db 584 ACGATGATTAGCAACATGCTTACAGAGAGAGAAAGACCGTGTGATGCCGATGGTG 643  
 Qy 363 GAGTAAGGTGATGACGATGCTGCTTATAGGAAGGCAACAGACGGTCTGACATGGATT 422  
 Db 644 GAGTAAGGTGATGACGATGCTGCTTATAGGAAGGCAACAGACGGTCTGACATGGATT 703  
 Qy 423 GGACGAACCACTAAATTCGCGATTGACAGAGATATTGATTTAAGTGGCTAGCTCGATACA 482  
 Db 704 GGACGAACCACTGATTCGCGATTGACAGAGATATTGATTTAAGTGGCTAGCTCGATACA 763  
 Qy 483 ATAAACGCCATTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCAATTC 523  
 Db 764 ATAAACGCCATTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCAATTC 804

RESULT 43  
 AAZ93331  
 ID AAZ93331 standard; DNA; 3310 BP.  
 XX  
 AC AAZ93331;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 DE Partial sequence of replication deficient adenoviral vector Ad5RSVRD.  
 XX  
 KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200014256-A1.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 03-SEP-1999; 99WO-US018834.  
 XX  
 PR 04-SEP-1998; 98US-00148275.  
 XX  
 PA (GENO-) GENOTHERAPEUTICS INC.  
 XX  
 PI Steiner MS, Lu Y;  
 XX  
 DR WPI; 2000-257001/22.  
 XX  
 PT Replication-deficient adenovirus type 5 expression vectors used for gene  
 therapy of cancer, especially prostate cancer, comprising an insertion of  
 PT nucleic acid encoding cytochrome p450 genes.  
 XX

PS Disclosure: Fig 10; 110pp; English.

Replication-deficient adenovirus type 5 expression vectors comprise an adenovirus genome with a deletion in the E1 and E2 region of the genome and an insertion within the region under the control of a Rous Sarcoma virus promoter can be used to induce chemotoxicity in tumour cells. Three such expression vectors are described, the inserted nucleic acids in each being the following: Vector (I) has an insertion of a nucleic acid encoding a cytochrome 2C9 p450 and is designated AdRSRV209 (ATCC VR-2628). Vector (II) has an insertion of a nucleic acid encoding a cytochrome 3A4 p450 and is designated AdRSRV344 (ATCC VR-2629). Vector (III) has an insertion of a nucleic acid encoding a nicotinamide adenine dinucleotide phosphate (NADPH) cytochrome p450 reductase and is designated AdRSRV362 (ATCC VR-2630). The chemotoxicity of a tumor cell can be induced by administering (I) and (II) or (I) and (III) into the tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell to a prodrug and then administering the prodrug which kills the cell, inducing its chemotoxicity. The method uses gene-directed enzyme prodrug therapy to transfer a drug susceptibility gene to the tumor which activates a nontoxic prodrug intratumorally so the released drug can kill the tumor cells containing the drug susceptibility gene. This sequence is designated region A of the vector AdRSRV262.

```
Query Match          75.1%; Score 393; DB 3; Length 3310;
Best Local Similarity 98.8%; Pred. No. 2.9e-127;
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

Qy	123	GCCTTCCGCAATGTACGGGCGAGATATTGCGCTATTCAGGGGACCTACGGTGTGTTTAGGCG	181
Db	404	GCSCCCCGATGTACGGGCGAGATATACGCGTATCTGTAGAGGGACGTAGGGTGTGTTTAGGCG	463
Qy	183	AAAAGCGGGGCTTCGGTTCTACGCGGTAGAGATCCCTCAGGATATAGTAGTTTCGCTT	242
Db	464	AAAGCGGGGCTTCGGTTGTACGCGTTAGGATCCCTCAGGATATAGTAGTTTCGCTT	523
Qy	243	TTGCATAGGAGGGGGAAATGTAGTCTTATTCGAATCTCTTGTAGTCTTGTGCACATGGTA	302
Db	524	TTGCATAGGAGGGGGAAATGTAGTCTTATTCGAATCTCTTGTAGTCTTGTGCACATGGTA	583
Qy	303	ACGATGAGTTAGCAACATGCTTACAGGAGAGAGAAAGACCGTGCATCCGATCGGATGGTG	362
Db	584	ACGATGAGTTAGCAACATGCTTACAGGAGAGAGAAAGACCGTGCATCCGATCGGATGGTG	643
Qy	363	GAAGTAAAGTGTACGATCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCACATGGATT	422
Db	644	GAAGTAAAGTGTACGATCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCACATGGATT	703
Qy	423	GGACGAACCACTAAATTCGCGAATCCGAGATATTGTATTTAAGTGGCTAGCTCGATACA	482
Db	704	GGACGAACCACTGAATTCGCGAATTCGAGATATTGTATTTAAGTGGCTAGCTCGATACA	763
Qy	483	ATAAGCGCAATTTGACCATTCACACATTTGGTGTGACCTC	523
Db	764	ATAAGCGCAATTTGACCATTCACACATTTGGTGTGACCTC	804

RESULT 44

AAZ93079  
ID AAZ93079 standard: DNA: 3311 bp.

XX  
MI  
AA3303

XX  
AC  
AAZ93079.

AC  
AH293073;  
YX

04-TUE-200

04-JUL-20  
DT  
VVXX  
Deserial  
DE

DE Partial s

XX	WO200014255-A1.
PN	
XX	
XX	16-MAR-2000.
PD	
XX	
XX	03-SEP-1999; 99WO-US018934.
PF	
XX	
XX	04-SEP-1998; 98US-00148275.
PR	
XX	
XX	(GENO-) GENOTHERAPEUTICS INC.
PA	
XX	
XX	Steiner MS, Lu Y;
PI	
XX	
XX	WPI; 2000-257001/22.
DR	
XX	
XX	Replication-deficient adenovirus type 5 expression vectors used for gene
PT	therapy of cancer, especially prostate cancer, comprising an insertion of
PT	nucleic acid encoding cytochrome p450 genes.
PT	
PT	
PS	Claim 18: Fig 11C: 110bp; English.
PS	

Replication-deficient adenovirus type 5 expression vectors comprise an adenovirus genome with a deletion in the E1 and E2 region of the genome and an insertion within the region under the control of a Rous Sarcoma virus promoter can be used to induce chemotoxicity in tumor cells. Three such expression vectors are described, the inserted nucleic acids in each being the following: Vector (I) has an insertion of a nucleic acid encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-2628). Vector (II) has an insertion of a nucleic acid encoding a cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector (III) has an insertion of a nucleic acid encoding a nicotinamide adenine dinucleotide phosphorylase (NADPH) cytochrome p450 reductase and is designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell can be induced by administering (I) and (III) or (II) and (III) into the tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell to a prodrug and then administering the prodrug which kills the cell, inducing its chemotoxicity. The method uses gene-directed enzyme prodrug therapy to transfer a drug susceptibility gene to the tumor which activates a nontoxic prodrug intratumorally so the released drug can kill the tumor cells containing the drug susceptibility gene. This sequence is designated region A of the vector Ad5RSVRED and is the sequence of the cytochrome NADPH p450 reductase

Query Match	75.1%	Score 393;	DB 3;	Length 3311;
Best Local Similarity	98.8%	Pred. No.	2.9e-127;	
Matches 396.	Conservative	0;	Mismatches 5;	Indels 0;
Gaps	0;			

Qy	123	GCCTCCGAGTGTACGGCCGAGATATTCGCGTATCTCAGAGGCACTAGGGTGTGTTTAGGGC	181
Db	404	GCGCCCGGATGTACGGCCGCAAGATATACGGCTATCTCAGAGGCACTAGGGTGTGTTTAGGGC	463
Qy	183	AAAAGCGGGCTTCGGTTGTACCGGGTTAGAGTCCCTCAGATATAGTAGTTTCGCTT	242
Db	464	AAAAGCGGGCTTCGGTTGTACCGGGTTAGAGTCCCTCAGATATAGTAGTTTCGCTT	523
Qy	243	TTGCAATAGGAGGGGGAATAGTAGTCTTATGCAATACATCTTGTAGTCTTGCAAAATCGTA	302
Db	524	TTGCAATAGGAGGGGGAATAGTAGTCTTATGCAATACATCTTGTAGTCTTGCAAAATCGTA	583
Qy	303	ACGATAGTGTAGCAACATGCCCTTACAAGGAGAGAAAAGCACCGTGCATCGCGATTGGTG	362
Db	584	ACGATAGTGTAGCAACATGCCCTTACAAGGAGAGAAAAGCACCGTGCATCGCGATTGGTG	643
Qy	363	GAAATAGTGTGACGATCGTGCCTTATTAGGAGAGCAACAGACGGGTCTGCACATGGATT	422
Db	644	GAAATAGTGTGACGATCGTGCCTTATTAGGAGAGCAACAGACGGGTCTGCACATGGATT	703
Qy	423	GGACGAACCACTAAATTCCGCAATTCCGAGATATTTGATTTTATAGTGCCTAGCTCGATACA	482
Db	704	GGACGAACCACTGAATTCGCAATTCGCAATTCGAGATATTTGATTTTATAGTGCCTAGCTCGATACA	763

QY 483 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
AAC89169  
Db 764 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 804

RESULT 45  
ID AAC89169 standard; DNA; 3885 BP.

XX AAC89169;  
XX  
DT 08-MAR-2001 (first entry)  
XX

XX ADRSVPHYDE region A coding sequence.

XX p-HYDE; cytostatic; gene therapy; apoptosis; leukaemia; prostate;  
XX tumour suppressor gene; DNA repair; cancer; melanoma; lymphoma;  
XX colorectal; pancreatic; breast; brain; gastric carcinoma; ds.

XX Unidentified.

XX WO200071564-A2.

XX 30-NOV-2000.

XX 01-MAY-2000; 2000WO-US011456.

XX 29-APR-1999; 99US-00302457.

XX 29-APR-1999; 99US-0131607P.

XX 08-FEB-2000; 2000US-00499817.

XX (UYTE-) UNIV TENNESSEE RES CORP.

XX Steiner MS, Wang C, Rinaldy A, Menon R;

XX WPI; 2001-032016/04.

XX New isolated nucleic acid encoding a mammalian p-Hyde protein of the p-Hyde family is useful for treating cancer, e.g. prostate cancer.

XX Disclosure; Fig 10; 171pp; English.

XX The present sequence is region A of ADRSVPHYDE. ADRSVPHYDE is an adenovirus vector expressing p-HYDE. p-HYDE induces susceptibility of a cancer cell to cell death. The p-HYDE gene is associated with the regression of tumour growth in vivo, the induction to susceptibility to apoptosis caused by UV or chemotherapy induced DNA damage and prevention of DNA repair with the upregulation of apoptosis as the result of UV damage and the failure to repair DNA. The present sequence may be used to treat cancer, preferably melanoma, lymphoma, leukaemia, prostate, colorectal, pancreatic, breast, brain or gastric carcinoma

XX Sequence 3885 BP; 847 A; 1039 C; 1063 G; 936 T; 0 U; 0 Other;

Query Match 75.1%; Score 393; DB 4; Length 3885;  
Best Local Similarity 98.8%; Pred. No. 3.2e-127;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGATGTACGGGCGAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
Db 404 GCGCCCGATGTACGGGCGAGATATACGGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 463

QY 183 AAAAGCGGGGCTTCGGTTGTACGCGGTATAGGAGTCCCTCAGGATATAGTATTCGCTT 242  
Db 464 AAAAGCGGGGCTTCGGTTGTACGCGGTATAGGAGTCCCTCAGGATATAGTATTCGCTT 523

QY 243 TTGCATAGGAGGGGGAATAGTCTTATGCATATCTTGTAGTCTTGCAATGGTA 302  
Db 524 TTGCATAGGAGGGGGAATAGTCTTATGCATATCTTGTAGTCTTGCAATGGTA 583

QY 303 ACGATGAGTTCGACATGCGCTTACAGGAGGAGAAAGCAGCGTCGATCCGATTTGGTG 362  
Db 584 ACGATGAGTTCGACATGCGCTTACAGGAGGAGAAAGCAGCGTCGATCCGATTTGGTG 643

QY 363 GAACTAAGGTGGTACGATCGTCTTATTAGGAGGCAACAGACGGGTCTGCATGGATT 422  
Db 644 GAACTAAGGTGGTACGATCGTCTTATTAGGAGGCAACAGACGGGTCTGCATGGATT 703  
QY 423 GGACGAACCACTAAATTCGGCATTCGAGAGATATTGTATTTAAGTCCCTAGCTGATACA 482  
Db 704 GGACGAACCACTAAATTCGGCATTCGAGAGATATTGTATTTAAGTCCCTAGCTGATACA 763  
QY 483 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
Db 764 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 804

RESULT 46

AAA09085

ID AAA09085 standard; DNA; 4487 BP.

XX AAA09085;

XX 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 10-AUG-2000 (first entry)

XX ADRSV-beta-galactosidase vector region A.

XX Region A; replication-deficient; vector; lacZ; beta-galactosidase;

XX Rous Sarcoma Virus; RSV; promoter; cytotoxicity; cytostatic; pro-drug;

XX prostate cancer; gene therapy; ss.

XX Human adenovirus type 5.

XX Rous sarcoma virus.

XX Escherichia coli.

XX Chimeric.

XX WO200020038-A1.

XX 13-APR-2000.

XX 01-OCT-1999; 99WO-US020907.

XX 02-OCT-1998; 98US-00165730.

XX (GENO-) GENOTHERAPEUTICS INC.

XX Steiner MS,

XX WPI; 2000-303646/26.

XX Inducing cellular cytotoxicity of tumor cell comprises introducing replication-deficient adenovirus type 5 expression vector containing gene encoding for enzyme having ability to convert nontoxic prodrug into cancer killing drug.

XX Claim 4; Fig 18B; 178pp; English.

XX This sequence comprises Region A of a replication-deficient adenovirus type 5 vector containing a lacZ gene (encoding beta-galactosidase (beta-gal)) under the control of the Rous Sarcoma Virus (RSV) promoter. Inducing cellular cytotoxicity of a tumor cell comprises introducing a replication-deficient adenovirus type 5 expression vector comprising a gene that encodes for an enzyme that has the ability to convert a non-toxic pro-drug into a cancer killing drug which then destroys cancer cells. The adenovirus genome preferably has a deletion in an E1 and E3 region and an insertion within the region of a nucleic acid encoding Escherichia coli beta-gal under the control of a promoter. The pro-drug active site is masked by beta-gal. Functional beta-gal is expressed from the vector so as to activate the pro-drug into an agent toxic to the cells. Beta-gal can be under the control of an RSV, probasin (PB), Prostate Specific Antigen (PSA) or Mouse Mammary Tumor Virus (MMTV) promoter. The vectors provide a novel way to treat prostate cancer by gene therapy. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 15-SEP-2003 to standardise OS field)

XX  
SQ Sequence 4487 BP; 1031 A; 1148 C; 1288 G; 1020 T; 0 U; 0 Other;  
Query Match 75.1%; Score 393; DB 3; Length 4487;  
Best Local Similarity 98.8%; Pred. No. 3.5e-127;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 123 GCTTCGCGATGTAACGGCCAGATATTCGCGTATCTGAGGGGACTAGGCGTGTGTTAGGCG 182  
DB 404 GCGCCCGAATGTAACGGCCAGATATACCGGCTATCTGAGGGGACTAGGCGTGTGTTAGGCG 463  
QY 183 AAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTTGCTT 242  
DB 464 AAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTTGCTT 523  
QY 243 TTGCTAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTA 302  
DB 524 TTGCTAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTA 583  
QY 303 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACGCTGCATGCGGATTTGGTG 362  
DB 584 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACGCTGCATGCGGATTTGGTG 643  
QY 363 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAACAGACGGGCTTGCATGGAAT 422  
DB 644 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAACAGACGGGCTTGCATGGAAT 703  
QY 423 GGACGACCACTAAATTCGGATTCGAGATATTTAGTGCCTAGCTCGATACA 482  
DB 704 GGACGACCACTAAATTCGGATTCGAGATATTTAGTGCCTAGCTCGATACA 763  
QY 483 ATAAAGCCATTGACCATTCACCAATTTGGTGTGCACCTC 523  
DB 764 ATAAAGCCATTGACCATTCACCAATTTGGTGTGCACCTC 804

RESULT 47  
AAAS9078  
ID AAAS9078 standard; DNA; 8238 BP.  
AC AAAS9078;  
XX  
XX 07-NOV-2000 (first entry)  
XX Nucleotide sequence of a plasmid.  
XX Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;  
XX ss.  
XX Synthetic.  
XX WO200042208-A1.  
XX  
XX 20-JUL-2000.  
XX  
XX 14-JAN-2000; 2000WO-EP000265.  
XX  
XX 14-JAN-1999; 99US-0115920P.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GBS MBH.  
XX (SCRI ) SCRIPPS RES INST.  
XX Nemerow GR, Von Seggern DJ, Hallenbeck FL, Stevenson SC;  
XX Skripchenko Y;  
XX WFI; 2000-476068/41.  
XX  
XX New nucleic acid comprising an adenovirus tripartite leader nucleotide  
XX for producing high-capacity and targeted vectors for adenovirus-based  
XX gene therapy.  
XX  
XX Disclosure; Page 195-198; 212pp; English.

XX The specification describes a nucleic acid molecule comprising an  
CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence  
CC comprising two different TPL exons or three same or different TPL exons.  
CC The nucleic acid is used to produce an adenovirus vector particle,  
CC deliver an exogenous gene to a target cell, pseudotype recombinant viral  
CC vectors, target an adenovirus vector to a cell, produce a modified  
CC adenovirus, deliver a heterologous gene to an animal and produce a  
CC gutless adenoviral vector particle. The present sequence represents a  
CC plasmid, which is used in the course of the invention  
XX  
SQ Sequence 8238 BP; 1762 A; 2156 C; 2340 G; 1980 T; 0 U; 0 Other;  
Query Match 75.1%; Score 393; DB 3; Length 8238;  
Best Local Similarity 98.8%; Pred. No. 4.7e-127;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 123 GCTTCGCGATGTAACGGCCAGATATTCGCGTATCTGAGGGGACTAGGCGTGTGTTAGGCG 182  
DB 404 GCGCCCGAATGTAACGGCCAGATATACCGGCTATCTGAGGGGACTAGGCGTGTGTTAGGCG 463  
QY 183 AAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTTGCTT 242  
DB 464 AAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTTGCTT 523  
QY 243 TTGCTAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTA 302  
DB 524 TTGCTAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTA 583  
QY 303 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACGCTGCATGCGGATTTGGTG 362  
DB 584 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACGCTGCATGCGGATTTGGTG 643  
QY 363 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAACAGACGGGCTTGCATGGAAT 422  
DB 644 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAACAGACGGGCTTGCATGGAAT 703  
QY 423 GGACGACCACTAAATTCGGATTCGAGATATTTAGTGCCTAGCTCGATACA 482  
DB 704 GGACGACCACTAAATTCGGATTCGAGATATTTAGTGCCTAGCTCGATACA 763  
QY 483 ATAAAGCCATTGACCATTCACCAATTTGGTGTGCACCTC 523  
DB 764 ATAAAGCCATTGACCATTCACCAATTTGGTGTGCACCTC 804

RESULT 48  
AAL56867  
ID AAL56867 standard; DNA; 33622 BP.  
XX  
XX AAL56867;  
XX  
XX 06-NOV-2003 (first entry)  
XX  
XX DNA sequence of the recombinant adenoviral Av3nBg vector.  
XX Fibre shaft modification; adenoviral vector; cell entry pathway; penton;  
XX CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;  
XX gene therapy; fibre knob; Av3nBg; ds.  
XX Human adenovirus type 5.  
XX Unidentified.  
XX WO2003062400-A2.  
XX  
XX 31-JUL-2003.  
XX  
XX 24-JAN-2003; 2003WO-US002295.  
XX  
XX 24-JAN-2002; 2002US-0350388P.  
XX 26-JUN-2002; 2002US-0391967P.  
XX  
XX (SCRI ) SCRIPPS RES INST.



PA (NOVS ) NOVARTIS AG.  
 XX  
 PI Kaleko M, Nemerow GR, Smith T, Stevenson SC;  
 XX WPI; 2003-627459/59.  
 DR  
 XX New modified adenovirus capsid protein, useful as a base vector for  
 PT producing redirected adenoviruses.  
 XX  
 PS Example 1; Page 156-165; 132pp; English.  
 XX  
 CC This invention relates to novel fibre shaft modifications in adenoviral  
 CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a  
 CC specific targeted tissue or organ, accordingly gene therapy requires the  
 CC ablation of normal virus tropism. If successful, systemic vector delivery  
 CC into a peripheral vein would be targeted to the desired location in the  
 CC body without any associated side effects, which would permit lower, less  
 CC toxic vector doses that are also potentially less immunogenic. The  
 CC present invention describes capsid modifications, specifically fibre  
 CC shaft mutations that when expressed on adenoviral particles ablates  
 CC binding to heparin sulphate proteoglycans (HSP) thus providing detargeted  
 CC vectors. Furthermore, when this is combined with modifications of other  
 CC adenoviral proteins involved in the cell entry pathway such as the fibre  
 CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors  
 CC become fully detargeted. As such, these fully ablated particles can be  
 CC used in vivo as base vectors for producing redirected adenoviruses with  
 CC the desired cell specificity. This polynucleotide sequence is the  
 CC recombinant E1, E2a and E3-deleted adenoviral vector (Avn99) that  
 CC encodes a nuclear localising beta-galactosidase, used in the  
 CC exemplification of the invention  
 XX  
 XX Sequence 33622 BP; 7857 A; 9539 C; 9277 G; 6949 T; 0 U; 0 Other;

Query Match 75.1%; Score 393; DB 8; Length 33622;  
 Best Local Similarity 98.8%; Pred. No. 9.8e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 123 GCTTCGCGATGTACGGCCAGATATTCCGCTATCTGAGGGACTAGGTGTGTTAGGCG 182  
 DB 396 GCGCCCGGATGTACGGCCAGATATTACCGGTATCTGAGGGACTAGGTGTGTTAGGCG 455  
 QY 183 AAAAGCGGGCTTCGGTTGTACCGGGTAGGAGTCCCTCAGGATATAGTAGTTGCGTT 242  
 DB 456 AAAAGCGGGCTTCGGTTGTACCGGGTAGGAGTCCCTCAGGATATAGTAGTTGCGTT 515  
 QY 243 TTCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGGTA 302  
 DB 516 TTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGGTA 575  
 QY 303 ACGATGAGTTAGCAATGCTTTACAGGAGAGAAAGCACCGTGATGCCGATTTGGTG 362  
 DB 576 ACGATGAGTTAGCAATGCTTTACAGGAGAGAAAGCACCGTGATGCCGATTTGGTG 635  
 QY 363 GAGTAAAGTGTAGTACGATGCTGCTTTATAGGAGGCAACAGCGGGTCTGACATGGAT 422  
 DB 636 GAAAGTAAAGTGTAGTACGATGCTGCTTTATAGGAGGCAACAGCGGGTCTGACATGGAT 695  
 QY 423 GAGCAACCACTTAATTCGCGATTCGAGAGATATTTTAAAGTGCCTAGCTGATACA 482  
 DB 696 GAGCAACCACTTAATTCGCGATTCGAGAGATATTTTAAAGTGCCTAGCTGATACA 755  
 QY 483 ATAAAGCCATTTGACCATTTACCATTTGATGATGTTGTCACCTC 523  
 DB 756 ATAAAGCCATTTGACCATTTACCATTTGATGATGTTGTCACCTC 796  
 RESULT 49  
 ID AAZ94163  
 XX  
 XX AAZ94163 standard; DNA; 34302 BP.  
 AC AAZ94163;  
 XX  
 DT 15-SEP-2003 (revised)

DT 19-JUN-2000 (first entry)  
 XX  
 DE Adenovirus vector Ad5RSVP16 used for prostate cancer gene therapy.  
 XX  
 XX Ad5RSVP16; adenovirus; vector; RSV; promoter; human; p16;  
 KW tumour suppressor gene; prostate cancer; gene therapy; ds.  
 XX  
 OS Human adenovirus type 5.  
 OS Rous sarcoma virus.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 XX Key Location/Qualifiers  
 FT promoter 410..805  
 FT /tag= a  
 FT misc\_feature 1055..2014  
 FT /tag= b  
 FT /note= "p16 sense cDNA"  
 XX  
 XX WO200014211-A1.  
 XX  
 XX 16-MAR-2000.  
 XX  
 XX 02-SEP-1999; 99WO-US018833.  
 XX  
 XX 02-SEP-1998; 98US-00145729.  
 XX  
 XX (GENO-) GENOTHERAPEUTICS INC.  
 PA  
 XX Steiner MS, Lu Y;  
 PI  
 XX WPI; 2000-256967/22.  
 DR  
 XX  
 XX Replication-deficient adenovirus type 5 expression vector, useful in gene  
 PT therapy of prostate cancer, comprises a nucleic acid encoding p16 under  
 PT the control of a Rous Sarcoma virus promoter.  
 XX  
 XX Disclosure; Fig 13; 118pp; English.  
 XX  
 CC The present sequence is that of replication-deficient adenovirus vector  
 CC Ad5RSVP16, deposited as ATCC VR 2626. The vector is a type 5 adenovirus  
 CC in which the E1 and E3 regions of the genome have been removed, and a p16  
 CC tumour suppressor gene (see AAZ94162) has been inserted under control of  
 CC a Rous sarcoma virus (RSV) promoter (see AAZ94161). Ad5RSVP16 can be used  
 CC in the gene therapy of prostate cancer to replace a missing, mutated or  
 CC inactivated p16 gene. In vitro, PC3 cells which were stably transfected  
 CC with the vector showed a 70% reduction in cell number. The vector also  
 CC inhibited growth of prostate cancer cells PPC-1, DU145 and PC3 in  
 CC culture. PPC-1 tumours grown in nude mice treated by a single injection  
 CC of Ad5RSVP16 had a marked reduction in tumour size when compared to  
 CC untreated control. The mice also survived for longer. Transduction rates  
 CC were over 90%, with transgene expression detectable in tumours for up to  
 CC 2 wk. (Updated on 15-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 34302 BP; 7995 A; 9797 C; 9303 G; 7207 T; 0 U; 0 Other;  
 Query Match 75.1%; Score 393; DB 3; Length 34302;  
 Best Local Similarity 98.8%; Pred. No. 9.9e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 123 GCTTCGCGATGTACGGCCAGATATTCCGCTATCTGAGGGACTAGGTGTGTTAGGCG 182  
 DB 404 GCGCCCGGATGTACGGCCAGATATTACCGGTATCTGAGGGACTAGGTGTGTTAGGCG 463  
 QY 183 AAAAGCGGGCTTCGGTTGTACCGGGTAGGAGTCCCTCAGGATATAGTAGTTGCGTT 242  
 DB 464 AAAAGCGGGCTTCGGTTGTACCGGGTAGGAGTCCCTCAGGATATAGTAGTTGCGTT 523  
 QY 243 TTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGGTA 302  
 DB 524 TTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGGTA 583  
 QY 303 ACGATGAGTTAGCAACATGCGCTTACAAAGGAGAGAAAGCACCGTGATCCGATTGGTG 362



Db 584 ACAGTGGTGTACGACATGCTTACAGGAGAGAAAAGCACCGTGGAAGCCGATGGTG 643  
 Qy 363 GAAGTAAGTGTGTACGATCGTGGCTTATTAGGAAGGCAACAGACGGGTCTGACATGAT 422  
 Db 644 GAAGTAAGTGTGTACGATCGTGGCTTATTAGGAAGGCAACAGACGGGTCTGACATGAT 703  
 Qy 423 GGAGCAACCACTAAATTCGCGATGCGAGATATGTTAAGTGCCTAGCTCGATACA 482  
 Db 704 GGAGCAACCACTAAATTCGCGATGCGAGATATGTTAAGTGCCTAGCTCGATACA 763  
 Qy 483 ATAAAGCCATTGTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 764 ATAAAGCCATTGTGACCAATTCACCAATTTGGTGTGCACCTC 804  
 RESULT 50  
 AAL56866  
 ID AAL56866 standard; DNA; 35211 BP.  
 AC AAL56866;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE DNA sequence of the recombinant adenoviral AvinBg vector.  
 XX  
 KW Fibre shaft modification; adenoviral vector; cell entry pathway; penton;  
 KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;  
 KW gene therapy; fibre knob; AvinBg; ds.  
 XX  
 OS Human adenovirus type 5.  
 OS Unidentified.  
 XX  
 EN WO2003062400-A2.  
 XX  
 PD 31-JUL-2003.  
 XX  
 PF 24-JAN-2003; 2003WO-US002295.  
 XX  
 PR 24-JAN-2002; 2002US-0350389P.  
 PR 26-JUN-2002; 2002US-0391967P.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 PI Kaleko M, Nemerow GR, Smith T, Stevenson SC;  
 XX  
 DR WPI; 2003-627459/59.  
 XX  
 PT New modified adenovirus capsid protein, useful as a base vector for  
 PT producing redirected adenoviruses.  
 XX  
 ES Example 1; Page 146-156; 132pp; English.  
 XX  
 CC This invention relates to novel fibre shaft modifications in adenoviral  
 CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a  
 CC specific targeted tissue or organ, accordingly gene therapy requires the  
 CC ablation of normal virus tropism. If successful, systemic vector delivery  
 CC into a peripheral vein would be targeted to the desired location in the  
 CC body without any associated side effects, which would permit lower, less  
 CC toxic vector doses that are also potentially less immunogenic. The  
 CC present invention describes capsid modifications, specifically fibre  
 CC shaft mutations that when expressed on adenoviral particles ablates  
 CC binding to heparin sulphate proteoglycans (HSP) thus providing defargeted  
 CC vectors. Furthermore, when this is combined with modifications of other  
 CC adenoviral proteins involved in the cell entry pathway such as the fibre  
 CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors  
 CC become fully defargeted. As such, these fully ablated particles can be  
 CC used in vivo as base vectors for producing redirected adenoviruses with  
 CC the desired cell specificity. This polynucleotide sequence is the  
 CC recombinant 51 and 53-deleted adenoviral vector (AvinBg) that encodes a  
 CC nuclear localising beta-galactosidase, used in the exemplification of the  
 CC invention

XX Sequence 35211 BP; 8136 A; 10028 C; 9704 G; 7343 T; 0 U; 0 Other;  
 SQ  
 Query Match 75.1%; Score 393; DB 8; Length 35211;  
 Best Local Similarity 98.8%; Pred. No. 1e-126;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Qy 123 GCTTCGGGATGTACGGGCGCATATTCGGGTATCTGAGGGGACTAGGGGTGTTTAGGCG 182  
 Db 510 GCGCCCGATGTACGGGCGCATATACGGGTATCTGAGGGGACTAGGGGTGTTTAGGCG 569  
 Qy 183 AAAAGCGGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGGATATAGTATTCGCTT 242  
 Db 570 AAAAGCGGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGGATATAGTATTCGCTT 629  
 Qy 243 TTGCATAGGAGGGGAAATGTAGTCTTATGCATATCTTGTAGTCTTGCAATGCTA 302  
 Db 630 TTGCATAGGAGGGGAAATGTAGTCTTATGCATATCTTGTAGTCTTGCAATGCTA 689  
 Qy 303 ACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTG 362  
 Db 690 ACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTG 749  
 Qy 363 GAACTAAGTGTGTACGATCGTGGCTTATTAGGAAGGCAACAGACGGGTCTGACATGATT 422  
 Db 750 GAACTAAGTGTGTACGATCGTGGCTTATTAGGAAGGCAACAGACGGGTCTGACATGATT 809  
 Qy 423 GGAGCAACCACTAAATTCGCGATGCGAGATATGTTAAGTGCCTAGCTCGATACA 482  
 Db 810 GGAGCAACCACTAAATTCGCGATGCGAGATATGTTAAGTGCCTAGCTCGATACA 869  
 Qy 483 ATAAAGCCATTGTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 870 ATAAAGCCATTGTGACCAATTCACCAATTTGGTGTGCACCTC 910  
 RESULT 51  
 AAZ29699  
 ID AAZ29699 standard; DNA; 11627 BP.  
 XX  
 AC AAZ29699;  
 XX  
 DT 22-MAR-2000 (first entry)  
 XX  
 DE Viral expression vector, RCASBP(A) construct.  
 XX  
 KW Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;  
 KW viral expression vector; RCASBP(A) construct; replication competent;  
 KW Bryan polymerase; BP; 'A' type envelope glycoprotein; mutant Src;  
 KW inflammatory disease; arthritis; rheumatoid arthritis; restenosis;  
 KW diabetic retinopathy; osteoporosis; cancer; ds.  
 XX  
 OS Synthetic.  
 OS Avian sarcoma virus.  
 XX  
 FH Key Location/Qualifiers  
 LTR 1..101  
 FT repeat\_unit 1..21  
 FT misc\_feature 22..101  
 FT CDS 372..2483  
 FT product= "gag protein"  
 FT note= "Proteins of nucleoprotein core of the virion"  
 FT mat\_peptide 372..902  
 FT label= gag p19\_peptide  
 FT misc\_recomb 388..391  
 FT note= "5'end unique sequence"  
 FT tag= a  
 FT tag= b  
 FT tag= c  
 FT tag= d  
 FT tag= e  
 FT tag= f



XX (PHEN-) PHENOGENE THERAPEUTICS INC.  
 XX Lanctot C, Gingras R, Gaumont M;  
 XX WPI; 2003-210275/20.  
 XX New vector having a nucleic acid sequence excisable by site-specific  
 PT recombination, useful for identifying or selecting exogenous nucleic  
 PT acids with desired features, e.g. nucleic acids encoding transcription  
 PT factors or kinases.  
 XX Claim 24; Page 103-112; 122pp; English.  
 XX The invention relates to novel vectors comprising nucleic acid sequences  
 CC excisable by a site-specific recombinase. The vectors or cells are useful  
 CC for identifying or selecting an exogenous nucleic acid having a desired  
 CC feature, e.g. nucleic acids encoding signalling molecules, transcription  
 CC factors or other proteins involved in changes of cell metabolism or  
 CC differentiation state (e.g. kinase or phosphatase). This polynucleotide  
 CC sequence represents the DNA of the vector RC77 relating to the invention  
 XX Sequence 16958 BP; 4816 A; 4210 C; 4125 G; 3807 T; 0 U; 0 Other;  
 SQ  
 Query Match 72.5%; Score 379; DB 7; Length 16958;  
 Best Local Similarity 98.5%; Pred. No. 6e-122;  
 Matches 393; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
 QY 126 TCGCGATGTACGGGCCAGATATCGCGTATCTGAGGGGACTAGGGHGTGTTAGCGGAAA 185  
 Db 14374 TAGCGATGTACGGGCCAGATATACGGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAA 14433  
 QY 186 AGCGGGCTTCGGTGTACGGGTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTG 245  
 Db 14434 AGCGGGCTTCGGTGTACGGGTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTG 14493  
 QY 246 CATAGGGAGGGGAAATAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATGTTAACG 305  
 Db 14494 CATAGGGAGGGGAAATAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATGTTAACG 14553  
 QY 306 ATGAGTTAGCAATGCTTCAAG 365  
 Db 14554 ATGAGTTAGCAATGCTTCAAG 14613  
 QY 366 GTRAGGTGTAGCATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGCAATTGGA 425  
 Db 14614 GTRAGGTGTAGCATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGCAATTGGA 14673  
 QY 426 CGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAT 484  
 Db 14674 CGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAT 14733  
 QY 485 AAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 14734 AAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 14772  
 RESULT 53  
 RAZ94161  
 ID AAZ94161 standard; DNB; 397 BP.  
 XX AAZ94161;  
 XX 19-JUN-2000 (first entry)  
 XX 395 Nucleic acid Rous sarcoma virus promoter.  
 DE Adenovirus; vector; RSV; promoter; prostate cancer; gene therapy;  
 KW tumour suppressor gene; p16; ss.  
 XX Rous sarcoma virus.  
 OS  
 XX WO200014211-A1.  
 PN

XX 16-MAR-2000.  
 PD 02-SEP-1999; 99WO-US018833.  
 XX 02-SEP-1998; 98US-00145729.  
 PR (GENO-) GENOTHERAPEUTICS INC.  
 XX Steiner MS, Lu Y;  
 XX WPI; 2000-256967/22.  
 DR Replication-deficient adenovirus type 5 expression vector, useful in gene  
 PT therapy of prostate cancer, comprises a nucleic acid encoding p16 under  
 PT the control of a Rous Sarcoma virus promoter.  
 XX Claim 1; Page 12; 118pp; English.  
 PS The present sequence is that of 395 nucleic acid Rous sarcoma virus (RSV)  
 CC promoter. A novel replication-deficient adenovirus type 5 expression  
 CC vector of the invention, termed AdRSVP16 (see AAZ94163), has a deletion  
 CC in an E1 and E3 region of the genome and contains a p16 tumour suppressor  
 CC gene under the control of the RSV promoter. The adenoviral vector is used  
 CC in the gene therapy of prostate cancer, in which p16 is frequently  
 CC inactivated. Gene therapy is used to replace a missing, mutated or  
 CC and/or progression of the tumour  
 XX Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;  
 SQ  
 Query Match 71.6%; Score 374.4; DB 3; Length 397;  
 Best Local Similarity 98.2%; Pred. No. 3.6e-121;  
 Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
 QY 129 CGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAAAGC 188  
 Db 1 CGATGTACGGGCCAGATATACCGGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAAAGC 60  
 QY 189 GGGGCTTCGGTGTACCGCGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCAT 248  
 Db 61 GGGGCTTCGGTGTACCGCGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCAT 120  
 QY 249 AGGAGAGGGGAAATAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATGTTAACGATG 308  
 Db 121 AGCCAGGGGGAAATAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATGTTAACGATG 180  
 QY 309 AGTTAGCAACATGCTTACAG 368  
 Db 181 AGTTAGCAACATGCTTACAG 240  
 QY 369 AGGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGCAATTGGAAGA 428  
 Db 241 AGGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGCAATTGGAAGA 300  
 QY 429 ACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAATAA 487  
 Db 301 ACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAATAA 360  
 QY 488 CGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 361 CGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 396  
 RESULT 54  
 AAA14719  
 ID AAA14719 standard; DNB; 397 BP.  
 XX AAA14719;  
 XX 08-AUG-2000 (first entry)  
 XX Nucleotide sequence of the Rous Sarcoma virus promoter.

XX Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;  
 KW replication-deficient adenovirus type 5; suicide gene therapy;  
 KW cancer cell; chemotherapy; beta-lactamase prodrug enzyme; prodrug TCM;  
 KW anticancer; tumor; leukemia; breast cancer; Wilms' tumor;  
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;  
 KW papillary adenocarcinoma; promoter; ss.  
 XX Rous sarcoma virus.  
 OS Rous sarcoma virus.  
 XX WO200020608-A1.  
 PN 13-APR-2000.  
 XX 01-OCT-1999; 99WO-US020908.  
 XX 02-OCT-1998; 98US-00165321.  
 XX (GENO-) GENOTHERAPEUTICS INC.  
 XX Steiner MS;  
 XX WPI; 2000-303788/26.  
 XX Treating cancer using viral vectors which encode enzymes that convert  
 PT inactive drugs to active cytotoxic agents, expression of the enzyme is  
 PT tissue specific therefore targeting the effects of the drug to tumor  
 PT cells.  
 XX Disclosure; Page 13-14; 130pp; English.  
 XX The specification describes a method for inducing cellular cytotoxicity  
 CC in tumor cells using replication-deficient adenovirus type 5 expression  
 CC vectors. The vectors comprise a sequence encoding a beta-lactamase under  
 CC the control of a Rous sarcoma virus in combination with a prodrug  
 CC conjugated to a toxic agent. Tissue specific expression of the enzyme  
 CC converts the inactive drugs into active cancer killing agents. The  
 CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-  
 CC lactamase sequence is inserted within this region. The vectors are used  
 CC for suicide gene therapy. This involves introducing genes into cancer  
 CC cells that encode enzymes capable of converting inactive drugs into  
 CC active cancer killing agents. If tissue specific promoters are coupled to  
 CC the prodrug enzymes, then production of the prodrug will be tissue  
 CC specific and targeted to the tumor. Therefore the cancer cells act as  
 CC their own factories to activate chemotherapy agents and commit suicide.  
 CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active  
 CC anticancer agent which is cytotoxic to cancer cells PPC-1. The method is  
 CC used to treat patients with cancers of the brain, bladder or prostate. It  
 CC may also be used to treat a range of other tumors such as leukemia,  
 CC breast cancer, Wilms' tumor, small cell lung carcinoma, Ewing's sarcoma,  
 CC colon carcinoma and papillary adenocarcinomas. The present sequence  
 CC represents the Rous Sarcoma virus promoter, which was used to  
 CC construct vectors of the invention  
 XX Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;  
 SQ Query Match 71.6%; Score 374.4; DB 3; Length 397;  
 Best Local Similarity 98.2%; Pred. No. 3.6e-121;  
 Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
 QY 129 CGATGACGGGCGAGATATCGCGGTATCTGAGGGGACTAGGGTGTGTTAGGGGAAAAGC 188  
 Db 1 CGATGTACGGGCGAGATATACGGGTATCTGAGGGGACTAGGGTGTGTTAGGGGAAAAGC 60  
 QY 189 GGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGATATAGTATGCTTTTGCAT 248  
 Db 61 GGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGATATAGTATGCTTTTGCAT 120  
 QY 249 AGGAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGTTAAAGCATG 308  
 Db 121 AGCCAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGTTAAAGCATG 180  
 QY 309 AGTTAGCAATCGCTTACAGAGAGAGAAAAGCACCGTGCATGCGGATTTGGTGAAGTA 368

Db 181 AGTTAGCAATCGCTTACAGAGAGAGAAAAGCACCGTGCATGCGGATTTGGTGAAGTA 240  
 QY 369 AGGTGGTACGATCGTCCCTTATTAGAGAGGCAACAGAGCGGTCTGACATGATGGACGA 428  
 Db 241 AGGTGGTACGATCGTCCCTTATTAGAGAGGCAACAGAGCGGTCTGACATGATGGACGA 300  
 QY 429 ACCACTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCCTAGCTCGATACATAAAA 487  
 Db 301 ACCACTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCCTAGCTCGATACATAAAA 360  
 QY 488 CGCCATTGACCATTCACCATTCGATGGTGCACCTC 523  
 Db 361 CGCCATTGACCATTCACCATTCGATGGTGCACCTC 396  
 RESULT 55  
 AAZ93077  
 ID AAZ93077 standard; DNA; 397 BP.  
 XX AC AAZ93077;  
 XX 04-JUL-2000 (first entry)  
 XX Rous Sarcoma Virus promoter sequence.  
 XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 KW Rous Sarcoma virus; HSV; chemotoxicity; transfection; sensitisation;  
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX Rous sarcoma virus.  
 OS Rous sarcoma virus.  
 XX WO200014256-A1.  
 PN 16-MAR-2000.  
 XX 03-SEP-1999; 99WO-US018834.  
 XX 04-SEP-1998; 98US-00148275.  
 XX (GENO-) GENOTHERAPEUTICS INC.  
 XX Steiner MS, Lu Y;  
 XX WPI; 2000-257001/22.  
 XX Replication-deficient adenovirus type 5 expression vectors used for gene  
 PT therapy of cancer, especially prostate cancer, comprising an insertion of  
 PT nucleic acid encoding cytochrome p450 genes.  
 XX Claim 8; Page 18; 110pp; English.  
 XX Replication-deficient adenovirus type 5 expression vectors comprise an  
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome  
 CC and an insertion within the region under the control of a Rous Sarcoma  
 CC virus promoter can be used to induce chemotoxicity in tumor cells. Three  
 CC such expression vectors are described, the inserted nucleic acids in each  
 CC being the following: Vector (I) has an insertion of a nucleic acid  
 CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-  
 CC 2828). Vector (II) has an insertion of a nucleic acid encoding a  
 CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector  
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 CC designated AdRSVRRED (ATCC VR-2630). The chemotoxicity of a tumor cell  
 CC can be induced by administering (I) and (III) or (II) and (III) into the  
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell  
 CC to a prodrug and then administering the prodrug which kills the cell,  
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 CC therapy to transfer a drug susceptibility gene to the tumor which  
 CC activates a nontoxic prodrug intratumorally so the released drug can kill  
 CC the tumor cells containing the drug susceptibility gene  
 XX Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 71.6%; Score 374.4; DB 3; Length 397;  
 Best Local Similarity 98.2%; Pred. No. 3.6e-121;  
 Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
 CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination  
 XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;  
 Query Match 71.3%; Score 372.8; DB 2; Length 37808;  
 Best Local Similarity 98.0%; Pred. No. 1.4e-113;  
 Matches 388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination  
 XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;  
 Query Match 71.3%; Score 372.8; DB 2; Length 37808;  
 Best Local Similarity 98.0%; Pred. No. 1.4e-113;  
 Matches 388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination  
 XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;

RESULT 56  
 AAX02780  
 ID AAX02780 standard; DNA; 37808 BP.  
 AC AAX02780;  
 XX  
 XX  
 DT 14-MAY-1999 (first entry)  
 DE Vector pMX-BG DNA.  
 XX  
 KW Vector pMX-BG; cloning; adenoviral minimal virus; AdMV; ITR; plasmid;  
 KW inverted terminal repeats; ITR; packaging signal; PSI; bacteriophage;  
 KW virus bank; genomic analysis; transgenic animal; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09902647-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 06-JUL-1998; 98WO-DB001940.  
 XX  
 PR 10-JUL-1997; 97DE-01029571.  
 PR 10-OCT-1997; 97DE-01044768.  
 XX  
 XX (HEPA-) HEPATOC GENTHERAPIE AG.  
 XX  
 XX Hillgenberg M, Loeser P, Schnieders F, Sandig V, Strauss M;  
 XX WPI; 1999-120851/10.  
 XX  
 XX New cloning vector for producing adenoviral minimal viruses - useful for  
 XX gene therapy or for preparation of virus banks and transgenic animals.  
 XX  
 XX Disclosure; Page 16-41, 57pp; German.  
 XX  
 CC This invention describes a novel cloning vector (A) for production of  
 CC adenoviral minimal viruses (AdMV). The vector is composed of two  
 CC adenoviral inverted terminal repeats (ITR) and a bacterial plasmid

CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination  
 XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;  
 Query Match 71.3%; Score 372.8; DB 2; Length 37808;  
 Best Local Similarity 98.0%; Pred. No. 1.4e-113;  
 Matches 388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination  
 XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;  
 Query Match 71.3%; Score 372.8; DB 2; Length 37808;  
 Best Local Similarity 98.0%; Pred. No. 1.4e-113;  
 Matches 388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination  
 XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;  
 Query Match 71.3%; Score 372.8; DB 2; Length 37808;  
 Best Local Similarity 98.0%; Pred. No. 1.4e-113;  
 Matches 388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination  
 XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;

RESULT 57  
 AAZ09997  
 ID AAZ09997 standard; cDNA; 5177 BP.  
 XX  
 AC AAZ09997;  
 XX  
 DT 03-DEC-1999 (first entry)  
 DE Bovine scavenger receptor class A (ScR)/avidin fusion protein cDNA.  
 XX  
 KW Scavenger receptor class A; ScR; avidin; fusion protein; bovine; ECD;  
 KW membrane-spanning domain; extracellular domain; biotin-binding activity;  
 KW endocytosis; ss.  
 XX  
 OS Synthetic.  
 OS Bos taurus.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1071..2269

```

FT FT /*tag= a
XX /product= "ScR/avidin fusion protein"
XX WO9942577-A2.
XX 26-AUG-1999.
XX 23-FEB-1999; 99WO-GB000546.
XX 23-FEB-1998; 98GB-00003757.
XX 24-JUN-1998; 98GB-00013653.
XX (EURO-) EUROGENE LTD.
XX Yla-Herttuala S, Kulomaa M, Lehtolainen P, Marjomaki V, Airenne K;
XX WPI; 1999-561345/47.
XX P-PSDB; AAY03098.
XX New fusion proteins having an extracellular domain with biotin-binding
XX activity, used to target biotinylated molecules to specific sites in
XX tissues.
XX Disclosure; Page 15-21; 23pp; English.
XX This invention describes a novel protein (A) which comprises a membrane-
XX spanning domain and an extracellular domain (ECD), where the ECD
XX comprises biotin-binding activity. Using the proteins or encoding nucleic
XX acid molecules it is possible to target biotinylated molecules to
XX specific sites in tissues. Molecules targeted in this way may be taken up
XX by the tissues or cells by endocytosis, allowing the molecules to exert
XX their effects within or on the cell. This sequence encodes a bovine
XX scavenger receptor class A/avidin fusion protein which is used in the
XX description of the invention
XX
XX Sequence 5177 BP; 1356 A; 1222 C; 1390 G; 1209 T; 0 U; 0 Other;
XX
XX Query Match 58.0%; Score 303.2; DB 2; Length 5177;
XX Best Local Similarity 99.0%; Pred. No. 1.7e-95;
XX Matches 305; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 216 TCCCTCAGGATAGTAGTTTCGCTTTGATAGGAGGGGAAATGATCTTATGCA 275
XX Db 3062 TCCCTCAGGATAGTAGTTTCGCTTTGATAGGAGGGGAAATGATCTTATGCA 3121
XX
XX QY 276 ATACTCTGTAGTCTTGCACATGTTAGCATGATGATTTAGCAACATGCTTACAGGAGAG 335
XX Db 3122 ATACTCTGTAGTCTTGCACATGTTAGCATGATGATTTAGCAACATGCTTACAGGAGAG 3181
XX
XX QY 336 AAAAGACCGTGCATCCGATGTTGGAAATGATAGTGGTACGATCGTGGCTTATTAGGA 395
XX Db 3182 AAAAGACCGTGCATCCGATGTTGGAAATGATAGTGGTACGATCGTGGCTTATTAGGA 3241
XX
XX QY 396 AGGCACACAGCGGTCTGACATGATTTGGACACACATGATTTCCGCTTGCAGAGATA 455
XX Db 3242 AGGCACACAGCGGTCTGACATGATTTGGACACACATGATTTCCGCTTGCAGAGATA 3301
XX
XX QY 456 TTGTATTAAAGTGGCTAGCTGCATACATAAATACCGCATTTGACCATTCACCAATTGGTG 515
XX Db 3302 TTGTATTAAAGTGGCTAGCTGCATACACACACCGCATTTGACCATTCACCAATTGGTG 3361
XX
XX QY 516 TGCACCTC 523
XX Db 3362 TGCACCTC 3369
XX
XX RESULT 58
XX AAD28272
XX ID AAD28272 standard; DNA; 7170 BP.
XX AC AAD28272;
XX XX
XX 22-APR-2002 (first entry)

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XX LSRNL vector.
XX LSRNL vector; pharmaceutical; industrial; diagnostic; screening; MoMuLV;
XX moloney murine leukemia virus; chimeric; hepatitis B virus; ds.
XX Hepatitis B virus.
XX Moloney murine leukemia virus.
XX Unidentified.
XX Chimeric.
XX Key Location/Qualifiers
XX LTR 1..589
XX /*tag= a
XX /*note= "MoMuLV 5' LTR"
XX misc_feature 659..897
XX /*tag= b
XX /*note= "Retroviral packaging region"
XX misc_feature 1034..1714
XX /*tag= c
XX /*note= "Hepatitis B surface antigen"
XX promoter 2279..2595
XX /*tag= d
XX /*note= "RSV promoter"
XX misc_feature 2951..3745
XX /*tag= e
XX /*note= "Neomycin phosphotransferase gene"
XX LTR 4537..5130
XX /*tag= f
XX /*note= "MoMuLV 3' LTR"
XX
XX WO200202738-A2.
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US020710.
XX
XX 03-JUL-2000; 2000US-0215925P.
XX (GALA-) GALA DESIGN INC.
XX
XX Brenel RD, Miller LU, Bleck GT, York D;
XX WPI; 2002-154737/20.
XX
XX The invention relates to a host cell comprising a genome having at least
XX two integrated integrating vectors. The integrating vectors comprise at
XX least one exogenous gene operably linked to a promoter. The host cell is
XX useful for producing a desired protein and for comparing protein
XX functions. The host cells comprises a reporter gene which is from gene
XX fluorescent protein, luciferase, beta-galactosidase and beta-lactamase,
XX and the assaying step further comprises detecting a signal from the
XX reporter gene. The desired protein includes proteins for pharmaceutical,
XX industrial, diagnostic and other purposes. The host cells is useful for
XX indirectly detecting the expression of a desired protein, comprising
XX providing the host cell transfected with a vector encoding a
XX polycistronic sequence comprising a signal protein and a desired protein
XX operably linked by an internal ribosome entry site (IRES), and culturing
XX the host cell under suitable conditions so that the signal protein and
XX the desired protein is produced, where the presence of signal protein
XX indicates the presence of desired protein. The present sequence is LSRNL
XX vector used in the invention. The vector comprises the following
XX elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV viral
XX packaging signal, hepatitis B surface antigen; RSV promoter; neomycin
XX phosphotransferase gene and 3' MoMuLV LTR
XX
XX Sequence 7170 BP; 1688 A; 1891 C; 1841 G; 1750 T; 0 U; 0 Other;
XX

```

Query Match 53.0%; Score 277; DB 6; Length 7170;  
 Best Local Similarity 97.4%; Pred. No. 3.6e-86;  
 Matches 303; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 215 GTCCCTCAGGATATAGTAGTTCGCTTTTGCATAGGAGGGGAAATGTAGTCTTATGC 274  
 DB 4320 GTCCCTCAGGATATAGTAGTTCGCTTTTGCATAGGAGGGGAAATGTAGTCTTATGC 4379

QY 275 AATACCTTGTAGTCTTGCACATGTATACGATGAGTAGCAACATGCTTACAGGAGA 334  
 DB 4380 AATACATTTGTAGTCTTGCACATGTATACGATGAGTAGCAACATGCTTACAGGAGA 4439

QY 335 GAAAGACACCTGTGATCCGATGTGTGAGTAACTGTAGTCTGCTTATTAG 394  
 DB 4440 GAAAGACACCTGTGATCCGATGTGTGAGTAACTGTAGTCTGCTTATTAG 4499

QY 395 AAGCAACAGAGCGGTCTGACATGATGAGACCACTAAATTCGCAATGCAAGAT 454  
 DB 4500 AAGCAACAGAGCGGTCTGACATGATGAGACCACTAAATTCGCAATGCAAGAT 4559

QY 455 -ATTGTATTAGTCTGCTGATACATATTAAGGCA--TTTGACCATTCACCATTT 511  
 DB 4560 AATTGTATTAGTCTGCTGATACATATTAAGGCA--TTTGACCATTCACCATTT 4619

QY 512 GGTGTGCACT 522  
 DB 4620 GGTGTGCACT 4630

RESULT 59  
 AAD28311  
 ID AAD28311 standard; DNA; 5130 BP.  
 XX AC AAD28311;  
 XX DT 22-APR-2002 (first entry)  
 XX DE LSRNL vector.  
 XX KW Regulatory element; vector; erythropoietin; growth hormone; insulin;  
 XX KW immunoglobulin; bone morphogenetic protein; interferon; interleukin;  
 XX KW superoxide dismutase; T-cell receptor; surface membrane protein;  
 XX KW viral antigen; transport protein; addressin; regulatory protein; MoMuLV;  
 XX KW moloney murine leukemia virus; chimeric; hepatitis B virus; ds.  
 XX OS Hepatitis B virus.  
 XX OS Moloney murine leukemia virus.  
 XX OS Unidentified.  
 XX OS Chimeric.

Key Location/Qualifiers  
 LTR 1..589 /\*tag= a  
 /\*note= "MoMuLV 5' LTR"  
 misc\_feature 659..897 /\*tag= b  
 /\*note= "Retroviral packaging region"  
 misc\_feature 1034..1714 /\*tag= c  
 /\*tag= "Hepatitis B surface antigen"  
 promoter 2279..2595 /\*tag= d  
 /\*note= "RSV promoter"  
 misc\_feature 2951..3745 /\*tag= e  
 /\*note= "Neomycin phosphotransferase gene"  
 LTR 4537..5130 /\*tag= f  
 /\*note= "MoMuLV 3' LTR"  
 PN W020202783-A2.

PD 10-JAN-2002.  
 XX 29-JUN-2001; 2001WO-US020714.  
 XX 03-JUL-2000; 2000US-0215851P.  
 XX (GALA-) GALA DESIGN INC.  
 XX Black GT;  
 XX WPI; 2002-154749/20.  
 DR Novel regulatory elements including nucleic acid encoding hybrid alpha-lactalbumin promoter or mutant RNA export element, for expressing one or more proteins e.g. antibodies, pharmaceutical proteins in host cells.  
 PT Example 1; Fig 12; 151pp; English.  
 XX The invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell. The invention further provides methods of indirectly detecting the expression of a protein of interest, comprising providing the host cell transfected with a vector encoding a polypeptidic sequence comprising a signal protein and a desired protein operably linked by an internal ribosome entry site (IRES), and culturing the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of elements and vectors of the invention are useful for the expressing an proteins of interest in a host cell. They are useful for producing an immunoglobulin (Ig), preferably secretory Ig. They are useful in the expression of one or more proteins such as erythropoietin, growth hormone, insulin, immunoglobulins, protein C, cytokines and their receptors, hormones, Von Willebrand factor, lung surfactant, serum albumins, DNase, vascular endothelial growth factor, receptors for hormones or growth factors, rheumatoid factors, nerve growth factors, CD proteins, osteoinductive factors, immunotoxins, bone morphogenetic protein, interferons, colony stimulating factors, interleukins, superoxide dismutase, T-cell receptors, surface membrane proteins, viral antigens, transport proteins, addressins, regulatory proteins, antibodies, chimeric proteins and their fragments. The vectors are particularly useful for expressing G protein coupled receptors and other transmembrane proteins. The retroviral vectors are useful for expressing proteins in mammalian tissue culture host cells, including rat fibroblast cells, bovine kidney cells and human kidney cells. The present sequence is LSRNL vector used in the invention. The vector comprises the following elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV viral packaging signal, hepatitis B surface antigen; RSV promoter; neomycin phosphotransferase gene and 3' MoMuLV LTR

XX Sequence 5130 BP; 1187 A; 1335 C; 1332 G; 1276 T; 0 U; 0 Other;  
 SQ Query Match 52.8%; Score 276.2; DB 6; Length 5130;  
 Best Local Similarity 93.7%; Pred. No. 5.8e-86;  
 Matches 310; Conservative 0; Mismatches 16; Indels 3; Gaps 2;

QY 195 TCGGTGTGACGGTTAGGAGTCCCTCAGGATATAGTAGTTCGCTTTTGCATAGGAG 254  
 DB 2260 TAGGGTGTGTCGCAACTGGATCCCTCAGGATATAGTAGTTCGCTTTTGCATAGGAG 2319

QY 255 GGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTTAAGTAGTTAG 314  
 DB 2320 GGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTTAAGTAGTTAG 2379

QY 315 CAACATGCTTTACAGGAGAGAAAAAGCACCGTCATGCCGATTTGGAGTAGTGG 374  
 DB 2380 CAACATGCTTTACAGGAGAGAAAAAGCACCGTCATGCCGATTTGGAGTAGTGG 2439

QY 375 TAGGATGTCCTTATTAGGAGCAACAGACGGCTTCACATGATTTGGACACCACT 434  
 DB 2440 TAGGATGTCCTTATTAGGAGCAACAGACGGCTTCACATGATTTGGACACCACT 2499

QY 435 AAATTCGCAATTCGAGAT-ATTGTATTATTAAGTSCCTAGCTCGATACATAAAGCCA- 492

Db 2500 GAATTCGGCAATTGCAGAGATAATTGATTAAAGTGCTAGCTCGATACAGCAAGCCAT 2559

QY 493 -TTTGACCAATTCACACCAATTGGTGGCACT 522

Db 2560 TTTTGACCAATTCACCAATTTGGTGGCACT 2590

RESULT 60

AA015665

ID AAS15665 standard; DNA; 262 BP.

XX AAS15665;

AC

XX 29-JAN-2002 (first entry)

DT

XX Human respiratory syncytial virus promoter.

DE

XX Bcdysone receptor; EcR; ligand binding domain; ds; retinoid X receptor;

KW RXRalpha; DNA-binding domain; RSV promoter; transactivation domain;

KW nuclear receptor; ultraspiracle; gene therapy; protein production;

KW antibody production; high throughput screening; HTS; transgenic plant;

KW transgenic animal.

XX

OS Human respiratory syncytial virus.

XX

PN WO200170816-A2.

PN

XX 27-SEP-2001.

PD

XX

XX 21-MAR-2001; 2001WO-US009050.

PF

XX 22-MAR-2000; 2000US-0191355P.

PR

XX 20-FEB-2001; 2001US-0269799P.

PR

XX (ROHM ) ROHM & HAAS CO.

PA

XX Palli SR, Kapitkaya MZ, Cress DE;

PI

XX WPI; 2001-656841/75.

DR

XX

XX Ecdysone and retinoid X receptor based inducible gene expression systems

PT for use in e.g. gene therapy, large scale production of proteins and cell

FT -based high-throughput screening assays.

PT

XX Example 1; Page 141; 144pp; English.

PS

XX The invention relates to Ecdysone and retinoid X receptor based inducible

CC gene expression systems useful for modulating gene expression in host

CC cells. The gene expression system encodes a polypeptide with a DNA-

CC binding domain recognizes a response element associated with a gene whose

CC expression is to be modulated and/or a ligand binding domain (LBD)

CC comprising a LBD from a nuclear receptor and a second gene expression

CC cassette capable of being expressed in a host cell comprising a

CC polynucleotide sequence encoding a second polypeptide comprising a trans-

CC activation domain and/or a LBD comprising a LBD from a nuclear receptor

CC other than ultraspiracle (USP) (the trans-activation domain is from a

CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor

CC or a USP receptor and the LBDs from the first and second polypeptides are

CC different and dimerize). The ecdysone and retinoid X receptor based

CC inducible gene expression systems useful for modulating gene expression

CC in host cells, for use in gene therapy, large scale production of

CC proteins and antibodies, cell-based high-throughput screening assays

CC (HTS), functional genomic and regulation of traits in transgenic plants

CC and animals. The present sequence represents promoter from human

CC respiratory syncytial virus (RSV) which is used in an inducible gene

CC expression system of the invention

XX

XX Sequence 262 BP; 79 A; 53 C; 64 G; 66 T; 0 U; 0 Other;

SQ

Query Match 49.2%; Score 257.2; DB 4; Length 262;

Best Local Similarity 98.9%; Pred. No. 6.2e-80;

Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGAGTTAGCAACAT 320

Db 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGAGTTAGCAACAT 60

QY 321 GCCTTACAAGGAGAGCAAAAGACCCGTGCATGCCGATTTGGTGGAGTAAGTGGTACAT 380

Db 61 GCCTTACAAGGAGAGCAAAAGACCCGTGCATGCCGATTTGGTGGAGTAAGTGGTACAT 120

QY 381 CGTGCCTTATTAGGAGGACACAGAGCGGCTCTGACATGGATTGACGACCACTAAATTC 440

Db 121 CGTGCCTTATTAGGAGGACACAGAGCGGCTCTGACATGGATTGACGACCACTAAATTC 180

QY 441 CGCATTCGACAGATATTGTATTTAAAGTGCTAGCTCGATACATAAAGCCATTGGACCA 500

Db 181 CGCATTCGACAGATATTGTATTTAAAGTGCTAGCTCGATACATAAAGCCATTGGACCA 240

QY 501 TTCACACATTTGGTGGCACT 522

Db 241 TTCACACATTTGGTGGCACT 262

RESULT 61

AAQ06310

ID AAQ06310 standard; DNA; 3188 BP.

XX

XX AAQ06310;

AC

XX 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX

XX Sequence of plasmid p79DBAM.

DE

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH 279..335

FT LTR

FT /\*tag= a

FT polyA\_signal 497..502

FT /\*tag= b

XX

XX EP393502-A.

PN

XX

XX 24-OCT-1990.

PD

XX

XX 11-APR-1990; 90EP-00106992.

PF

XX 19-APR-1989; 89EP-00810295.

PR

XX (HOFF ) HOFFMANN-LA ROCHE AG.

PA

XX Fountoulak M, Garotta G, Stuber D;

PI

XX WPI; 1990-322042/43.

DR

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,

PT chronic inflammations, etc.

PT

XX Disclosure; Fig 49; 174pp; English.

PS

XX IFN-gamma is a therapeutically active agent in the treatment of

CC autoimmune disease, allograft transplant rejections, multiple sclerosis,

CC chronic inflammations and delayed hypersensitivity. It is also useful in

CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

CC [Updated on 25-MAR-2003 to correct PR field.]

XX

XX Sequence 3188 BP; 797 A; 774 C; 882 G; 735 T; 0 U; 0 Other;

SQ

Query Match 48.4%; Score 253; DB 2; Length 3188;

Best Local Similarity 93.2%; Pred. No. 6.9e-78;

Matches 288; Conservative 0; Mismatches 15; Indels 6; Gaps 2;



CC 220 CTCAGGATATAGTATGCTTTCGCTTTTCATAGGGGGGAAATGATGCTTATGCAATAC 279  
 CC 5 CTCAGGATATAGTATGCTTTCGCTTTTCATAGGGGGGAAATGATGCTTATGCAATAC 64  
 CC 280 TCTTGTAGTCTTGCACATG-----GTAACGATGATGTTAGCAACATGCTTACAAGGAGA 334  
 CC 65 TCTTGTAGTCTTGCACATGCTTATGTAACGATGATGTTAGCAACATGCTTACAAGGAGA 124  
 CC 335 GAAAACACCGTGCATCCGATTCGCTTGGAGTGAAGTGTAGCATGCTTATGAGG 394  
 CC 125 GAAAACACCGTGCATCCGATTCGCTTGGAGTGAAGTGTAGCATGCTTATGAGG 183  
 CC 395 AAGCAACACGCGGTCTGACATGGAATGGAACCACTAAATTCGCGATTGCAGAGAT 454  
 CC 184 AAGCAACACGCGGTCTGACATGGAATGGAACCACTAAATTCGCGATTGCAGAGAT 243  
 CC 455 ATTGTATTTAAGTGTGCTAGCTCGATACAAATAAAGCCCATTTGACCAATTCGAT 514  
 CC 244 ATTGTATTTAAGTGTGCTAGCTCGATACAAATAAAGCCCATTTGACCAATTCGAT 303  
 CC 515 GTGCACCTC 523  
 CC 304 GTGCACCTC 312

Query Match 48.4%; Score 253; DB 2; Length 3276;  
 Best Local Similarity 93.2%; Pred. No. 7e-78;  
 Matches 288; Conservative 0; Mismatches 15; Indels 6; Gaps 2;  
 QY 220 CTCAGGATATAGTATGCTTTCGCTTTTCATAGGGGGGAAATGATGCTTATGCAATAC 279  
 Db 5 CTCAGGATATAGTATGCTTTCGCTTTTCATAGGGGGGAAATGATGCTTATGCAATAC 64  
 QY 280 TCTTGTAGTCTTGCACATG-----GTAACGATGATGTTAGCAACATGCTTACAAGGAGA 334  
 Db 65 TCTTGTAGTCTTGCACATGCTTATGTAACGATGATGTTAGCAACATGCTTACAAGGAGA 124  
 QY 335 GAAAACACCGTGCATCCGATTCGCTTGGAGTGAAGTGTAGCATGCTTATGAGG 394  
 Db 125 GAAAACACCGTGCATCCGATTCGCTTGGAGTGAAGTGTAGCATGCTTATGAGG 183  
 QY 395 AAGCAACACGCGGTCTGACATGGAATGGAACCACTAAATTCGCGATTGCAGAGAT 454  
 Db 184 AAGCAACACGCGGTCTGACATGGAATGGAACCACTAAATTCGCGATTGCAGAGAT 243  
 QY 455 ATTGTATTTAAGTGTGCTAGCTCGATACAAATAAAGCCCATTTGACCAATTCGAT 514  
 Db 244 ATTGTATTTAAGTGTGCTAGCTCGATACAAATAAAGCCCATTTGACCAATTCGAT 303  
 QY 515 GTGCACCTC 523  
 Db 304 GTGCACCTC 312

RESULT 62  
 AAQ06311  
 ID AAQ06311 standard; DNA; 3276 BP.  
 XX  
 AC AAQ06311;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 DE Sequence of plasmid p238BGL.  
 XX  
 KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 EH Key Location/Qualifiers  
 FT CDS 243..426  
 FT /\*tag= b  
 FT Sig-peptide 243..405  
 FT /\*tag= c  
 FT /\*label= S.P.1  
 FT LTR 279..242  
 FT polyA\_signal /\*tag= a  
 FT 585..590  
 FT /\*tag= d  
 XX  
 PN EP393502-A.  
 XX  
 XX 24-OCT-1990.  
 XX  
 XX 11-APR-1990; 90EP-00106992.  
 XX  
 XX 19-APR-1989; 89EP-00810295.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX  
 XX Fountoulak M, Garotta G, Stuber D;  
 XX  
 XX WPI; 1990-322042/43.  
 XX P-PSDB; AAR07066.  
 XX  
 XX Soluble interferon-gamma receptors - for treating auto-immune diseases,  
 PT chronic inflammations, etc.  
 XX  
 XX Disclosure; Fig 51; 174pp; English.  
 XX

CC IFN-gamma is a therapeutically active agent in the treatment of  
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,  
 CC chronic inflammations and delayed hypersensitivity. It is also useful in  
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 U; 0 Other;  
 Query Match 48.4%; Score 253; DB 2; Length 3276;  
 Best Local Similarity 93.2%; Pred. No. 7e-78;  
 Matches 288; Conservative 0; Mismatches 15; Indels 6; Gaps 2;  
 QY 220 CTCAGGATATAGTATGCTTTCGCTTTTCATAGGGGGGAAATGATGCTTATGCAATAC 279  
 Db 5 CTCAGGATATAGTATGCTTTCGCTTTTCATAGGGGGGAAATGATGCTTATGCAATAC 64  
 QY 280 TCTTGTAGTCTTGCACATG-----GTAACGATGATGTTAGCAACATGCTTACAAGGAGA 334  
 Db 65 TCTTGTAGTCTTGCACATGCTTATGTAACGATGATGTTAGCAACATGCTTACAAGGAGA 124  
 QY 335 GAAAACACCGTGCATCCGATTCGCTTGGAGTGAAGTGTAGCATGCTTATGAGG 394  
 Db 125 GAAAACACCGTGCATCCGATTCGCTTGGAGTGAAGTGTAGCATGCTTATGAGG 183  
 QY 395 AAGCAACACGCGGTCTGACATGGAATGGAACCACTAAATTCGCGATTGCAGAGAT 454  
 Db 184 AAGCAACACGCGGTCTGACATGGAATGGAACCACTAAATTCGCGATTGCAGAGAT 243  
 QY 455 ATTGTATTTAAGTGTGCTAGCTCGATACAAATAAAGCCCATTTGACCAATTCGAT 514  
 Db 244 ATTGTATTTAAGTGTGCTAGCTCGATACAAATAAAGCCCATTTGACCAATTCGAT 303  
 QY 515 GTGCACCTC 523  
 Db 304 GTGCACCTC 312

RESULT 63  
 AAQ06309  
 ID AAQ06309 standard; DNA; 3383 BP.  
 XX  
 AC AAQ06309;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 DE Sequence of plasmid p76BGL.  
 XX  
 KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 EH Key Location/Qualifiers  
 FT LTR 279..504  
 FT /\*tag= a  
 FT CDS 505..540  
 FT /\*tag= b  
 FT polyA\_signal 692..697  
 FT /\*tag= c  
 XX  
 PN EP393502-A.  
 XX  
 XX 24-OCT-1990.  
 XX  
 XX 11-APR-1990; 90EP-00106992.  
 XX  
 XX 19-APR-1989; 89EP-00810295.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX  
 XX Fountoulak M, Garotta G, Stuber D;  
 XX





RESULT 67  
AAC92489  
ID AAC92489 standard; DNA; 858 BP.  
XX  
AC AAC92489;  
XX  
DT 26-MAR-2001 (first entry)  
XX  
DE Fragment of RSV DNA including tandem repeat LTR and non-coding region.  
XX  
KW Integrase; transgenic animal; transgenic bird; gene therapy; cancer; ds.  
XX  
OS Rous sarcoma virus.  
XX  
PN WO200075342-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 27-APR-2000; 2000WO-JP002785.  
XX  
PR 04-JUN-1999; 99JP-00158351.  
XX  
PA (NIPP) NIPPON INST BIOLOGICAL SCIENCE.  
XX  
PI Katsumata A, Hoshi S, Ihara T, Ueda S;  
XX  
DR WPI; 2001-061729/07.  
XX  
XX Plasmid vector for efficient insertion of foreign DNA into host cells to  
PT give transforms with stable quality, useful e.g. in producing DNA  
PT vaccines on large scale, and in gene therapy with ease and safely and  
PT without pathogenicity.  
XX  
PS Disclosure; Page 88-99; 94pp; Japanese.  
XX  
XX This invention relates to a vector which consists of an integrase gene, a  
CC regulatory region of DNA involved in the expression of the integrase  
CC gene, and a DNA fragment constituting a recognition region used in the  
CC catalysis of the integrase in the integrase reaction. The invention  
CC includes methods for the production of transgenic animals and birds using  
CC the vector of the invention. The plasmid vector can be for inserting  
CC foreign DNA into host cells to yield transformants. The transformants may  
CC be useful in producing DNA vaccines, and in gene therapy against cancer,  
CC congenital genetic diseases or infections. The present sequence  
CC represents a fragment of DNA from Rous sarcoma virus, including tandem  
CC repeat LTRs and adjacent non-coding region. The DNA fragment is used in  
CC the production of the vector of the invention.  
XX  
SQ Sequence 858 BP; 215 A; 202 C; 246 G; 195 T; 0 U; 0 Other;  
Query Match 40.6%; Score 212.2; DB 5; Length 858;  
Best Local Similarity 88.1%; Pred. No. 8.5e-64;  
Matches 260; Conservative 0; Mismatches 18; Indels 17; Gaps 2;  
QY 245 GCATAGGAGGGGAAATAGTCTTTATGCAATACTCTTGTAGTCTTCCACATG----- 299  
DB 200 GCAGAGGCTTCAATTAATAGTCTTTATGCAATACTCTTGTAGTCTTCCACATGCTTAT 259  
QY 300 GTAAAGTATGATAGTACGACGCTTACAGGAGAGAAAGCAGCCGTCGTCGCAATG 359  
DB 260 GTAAAGTATGATAGTACGACGCTTACAGGAGAGAAAGCAGCCGTCGTCGCAATG 319  
QY 360 GTGGAATAGGT-----GGTACGATCGCTCTTATAGGAGGCAACAGAG 407  
DB 320 GTGGAATAGGTGATGATCTAGTACGATCGTCTTATAGGAGGCAACAGAG 379  
QY 408 GGTCTGACATGATGGAAGCAACCACTAAATCCGCAATGCAAGATATTGATTTAAT 467  
DB 380 GGTCTAAGCGATGGAAGCAACCACTAAATCCGCAATGCGAGATATTGATTTAAT 439  
QY 468 GCCTAGCTGATACATTAAGCGCATTTGACCATTCACCAATTTGGTGGCACT 522  
DB 440 GCCTAGCTGATACATTAAGCGCATTTTACCATTCACCAATTTGGTGGCACT 494

RESULT 68  
AA77359  
ID AA77359 standard; DNA; 9542 BP.  
XX  
AC AA77359;  
XX  
DT 09-AUG-1999 (first entry)  
XX  
DE Polynucleotide sequence of 987 BB neo.  
XX  
KW Nucleic acid identification; exogenous protein; gene sorting;  
XX growth factor; membrane receptor; sindbis virus; ss.  
XX  
OS Synthetic.  
XX  
PN WO925876-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 17-NOV-1998; 98WO-US024520.  
XX  
PR 17-NOV-1997; 97US-00972218.  
XX  
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.  
XX  
PI Bailey JE, Renner WA, Orberger GH, Koller D;  
XX  
DR WPI; 1999-357620/30.  
XX  
XX Isolating genes encoding proteins with selected properties, useful for  
PT identifying therapeutic agents or targets.  
XX  
PS Disclosure; Fig 13A-C; 136pp; English.  
XX  
XX The invention relates to the identification of a recombinant nucleic acid  
CC encoding an exogenous protein having a selected property. The method  
CC comprises preparing a population of eukaryotic host cells, culturing the  
CC cells under suitable conditions and identifying cells that contain the  
CC recombinant nucleic acid. The method is used to sort genes according to  
CC the type of proteins they express, and also to identify new ligand/  
CC receptor interactions. Typical applications of the nucleic acid and the  
CC exogenous protein are in isolation of new growth factors, cytokines,  
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of  
CC which may be useful as therapeutic agents or therapeutic targets, e.g.  
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell  
CC proliferation or metabolic processes etc. The protein can also be used as  
CC screen for specific modulators. The nucleic acid can also be used as  
CC sources of therapeutic antisense or ribozyme sequences. The method allows  
CC the protein (rather than a partial DNA sequence) to be isolated and,  
CC since a wide range of cells can be used, they can be expressed with the  
CC correct glycosylation pattern  
XX  
SQ Sequence 9542 BP; 2463 A; 2516 C; 2387 G; 2176 T; 0 U; 0 Other;  
Query Match 39.2%; Score 205.2; DB 2; Length 9542;  
Best Local Similarity 98.6%; Pred. No. 8.8e-61;  
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 261 ATGTAGTCTTATGCAATACTCTTGTAGTCTTGTGCAACATGTTAGTGTAGTACAT 320  
DB 665 ATCCAGTCTTATGCAATACTCTTGTAGTCTTGTGCAACATGTTAGTGTAGTACAT 724  
QY 321 GCCTTACAGGAGAGAAAGCCCGTCGATCCGATGTCGAGTAGTGTAGTGTAGTAT 380  
DB 725 GCCTTACAGGAGAGAAAGCCCGTCGATCCGATGTCGAGTAGTGTAGTGTAGTAT 784  
QY 381 GGTCCCTTATTAGGAAGCAACAGACGGGTCTGTGATGGATTGGACGACCACTAAATTC 440  
DB 785 GGTCCCTTATTAGGAAGCAACAGACGGGTCTGTGATGGATTGGACGACCACTAAATTC 844  
QY 441 GGTCCCTTATTAGGAAGCAACAGACGGGTCTGTGATGGATTGGACGACCACTAAATTC 470

Db	845	CGCATTGCAGAGATATTGTTAAGTGCC	874
Db	321	GCCTTACAGAGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGAT	380
Db	725	GCCTTACAGAGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGAT	784
Qy	381	CGTGCCCTTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAAACCACTAAATTC	440
Db	785	CGTGCCCTTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAAACCACTAAATTC	844
Qy	441	CGCATTGCAGAGATATTGTTAAGTGCC	470
Db	845	CGCATTGCAGAGATATTGTTAAGTGCC	874
RESULT 70			
AAZ27850			
ID	AAZ27850	standard; cDNA; 11282 BP.	
XX	AAZ27850;		
AC	AAZ27850;		
XX	23-DEC-1999	(first entry)	
DT	XX		
XX	Complete cDNA sequence of pCYTts.		
DE	XX		
XX	Gene expression system; cis-acting element; gene therapy;		
KW	temperature-sensitive RNA-dependent RNA polymerase;		
KW	inducible alphaviral gene expression system; pCYTts;		
KW	hormone-based gene control system; tetracycline gene control system; ss.		
XX	Synthetic.		
OS	XX		
XX	WO9950432-A1.		
PN	XX		
XX	07-OCT-1999.		
PD	XX		
XX	25-MAR-1999;	99WO-IB000523.	
PF	XX		
XX	27-MAR-1999;	98US-0079562P.	
PR	XX		
XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.		
PA	(RENN/) RENNER W A.		
PA	(NIEB/) NIEBA L.		
PA	(BOOR/) BOORSMA M.		
XX	Renner WA, Nieba L, Boorsma M;		
PI	XX		
XX	WPI; 1999-591327/50.		
DR	XX		
XX	A new system to regulate gene expression in eukaryotic cells.		
PT	XX		
PS	Claim 15; Fig 3; 99pp; English.		
XX	This sequence represents the complete cDNA sequence for the vector		
CC	pCYTts. The invention relates to a DNA molecule comprising a		
CC	polynucleotide (i) encoding an RNA molecule. The encoded RNA comprises:		
CC	(a) at least one cis-acting element; (b) an open reading frame (ORF1)		
CC	encoding a non-cytopathic, temperature-sensitive RNA-dependent RNA		
CC	polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF		
CC	(ORF2) that is in a translatable format after RNA-dependent RNA		
CC	replication event(s); (ii) a sequence complementary to the ORF2; or (iii)		
CC	a sequence encoding an untranslated RNA molecule. The pCYTts sequence is		
CC	an example of the DNA molecule, and is an inducible alphaviral gene		
CC	expression system. The invention is used in gene therapy and recombinant		
CC	technology to regulate expression of introduced genes. The invention does		
CC	not have the problems of toxicity and/or high basal level expression		
CC	associated with prior art tetracycline-based and hormone-based gene		
CC	control systems		
XX	Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;		
SQ	Query Match	39.2%; Score 205.2; DB 2; Length 11282;	
	Best Local Similarity	98.6%; Pred. No. 9.6e-61;	
	Matches	207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	

QY 261 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACAT 320  
 Db |||||  
 664 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACAT 723  
 QY 321 GCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAAGTAAAGTGTGACGAT 380  
 Db |||||  
 724 GCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAAGTAAAGTGTGACGAT 783  
 QY 381 CGTGCCTTATTAGGAAGGACACAGACCGGTCTGACATGGATTGGACGAACCACTAAATTC 440  
 Db |||||  
 784 CGTGCCTTATTAGGAAGGACACAGACCGGTCTGACATGGATTGGACGAACCACTAAATTC 843  
 QY 441 CGCATTCGACAGATATTTGATTAAAGTGCC 470  
 Db |||||  
 844 CGCATTCGACAGATATTTGATTAAAGTGCC 873

RESULT 71  
 AAD04741  
 ID AAD04741 standard; cDNA; 11282 BP.  
 XX  
 AC AAD04741;  
 XX  
 DT 17-JUL-2001 (first entry)  
 XX  
 DE Alphaviral vector pCYTts cDNA.  
 XX  
 KW pCYTts; alphaviral vector; vaccine; therapy; cancer; antiparasitic;  
 KW antimalarial; anticancer; anti-HIV; antiviral; infectious disease;  
 KW human immunodeficiency virus; HIV; influenza; passive immunisation;  
 KW carcinoma; liver; skin; stomach; ovarian tumour; ss.  
 XX  
 OS Rous sarcoma virus.  
 OS Alphavirus.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 PN WO200130989-A2.  
 XX  
 PD 03-MAY-2001.  
 XX  
 XX 26-OCT-2000; 2000WO-IB001557.  
 XX  
 XX 27-OCT-1999; 99US-0161796P.  
 XX  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (RENN/) RENNER W A.  
 PA (NIEB/) NIEBA L.  
 XX  
 PI Renner WA, Nieba L;  
 XX  
 DR WPI; 2001-308631/32.  
 XX  
 XX Preparing alphaviral vectors with mutations in a selected gene, for use  
 PT as vaccines, particularly against pathogens that mutate rapidly,  
 PT comprises replicating in the presence of a nucleoside analog.  
 XX  
 PS Claim 6; Fig 3; 103pp; English.

XX The present invention relates to a method for preparing viral vectors  
 CC which comprises inserting a gene of interest into an alphaviral vector  
 CC such as pCYTts, pSinpRep and replicating the vector in the presence of  
 CC alphaviral replicase and nucleoside analogues (5'-azacytidine (AZT), FU-  
 CC 5'-fluorouridine) to produce a modified gene of interest. The replication  
 CC is repeated until the modified gene in 90 % of the vector population  
 CC contain a mutation in the modified gene which is 90-99 % identical with  
 CC the gene of interest. The vector populations are used in vaccines for  
 CC treatment or prevention of a wide variety of infectious diseases (viral  
 CC or parasitic, e.g. human immunodeficiency virus (HIV), influenza,  
 CC Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach  
 CC carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the  
 CC mutant populations will therefore be effective against viral escape  
 CC mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins

CC are correctly glycosylated. Antisera raised against the vaccines can be  
 CC used for passive immunisation. The present cDNA sequence is an alphaviral  
 CC vector pCYTts. The vector contains Rous Sarcoma Virus promoter, cis-  
 CC acting sequence elements, non-structural proteins 1-4, gene of interest,  
 CC alphavirus subgenomic promoter, ampicillin resistance marker for  
 CC selection and a CoIE1 sequence for bacterial amplification  
 XX  
 SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;  
 Query Match 39.2%; Score 205.2; DB 4; Length 11282;  
 Best Local Similarity 98.6%; Pred. No. 9.6e-61;  
 Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 261 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACAT 320  
 Db |||||  
 664 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACAT 723  
 QY 321 GCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAAGTAAAGTGTGACGAT 380  
 Db |||||  
 724 GCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAAGTAAAGTGTGACGAT 783  
 QY 381 CGTGCCTTATTAGGAAGGACACAGACCGGTCTGACATGGATTGGACGAACCACTAAATTC 440  
 Db |||||  
 784 CGTGCCTTATTAGGAAGGACACAGACCGGTCTGACATGGATTGGACGAACCACTAAATTC 843  
 QY 441 CGCATTCGACAGATATTTGATTAAAGTGCC 470  
 Db |||||  
 844 CGCATTCGACAGATATTTGATTAAAGTGCC 873  
 RESULT 72  
 AAF84024  
 ID AAF84024 standard; cDNA; 11282 BP.  
 XX  
 AC AAF84024;  
 XX  
 DT 22-AUG-2001 (first entry)  
 XX  
 DE Complete cDNA sequence of plasmid pCYTt.  
 XX  
 KW pCYTt; cellular; taxol; gene therapy; RNA replication; endogenous gene;  
 KW ss.  
 XX  
 OS Synthetic.  
 OS  
 XX WO200142442-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 XX 08-DEC-2000; 2000WO-IB001841.  
 XX  
 XX 10-DEC-1999; 99US-0169988P.  
 XX  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 XX  
 PI Hennecke F, Renner WA;  
 XX  
 DR WPI; 2001-381672/40.  
 XX  
 XX Modifying endogenous target gene expression in eukaryotic cell for  
 PT performing gene therapy, involves inserting exogenous polynucleotides in  
 PT gene to produce recombinant eukaryotic host cell and culturing the cell.  
 XX  
 PS Disclosure; Fig 8A-D; 131pp; English.  
 XX  
 CC The invention relates to a method of modifying expression characteristics  
 CC of an endogenous target gene within a genome of a eukaryotic cell or  
 CC producing a polypeptide encoded by the target gene of a eukaryotic cell.  
 CC The method involves inserting exogenous polynucleotides in 5' and 3'  
 CC regions flanking the coding region of target gene to produce a  
 CC recombinant eukaryotic host cell, and culturing the cell. The method is  
 CC useful for producing cells which exhibit increased expression of  
 CC endogenous genes which lead to the production of additional products, and

CC for amplifying endogenous genes involved in the production of cellular  
CC products such as taxol. The method is also useful for producing  
CC biological products, and their derivatives, and for regulating the  
CC activity of target genes by modifying the expression of regulatory  
CC proteins involved in the regulation of the target genes. The method or a  
CC DNA vector system is useful for performing gene therapy on an individual  
CC (e.g., domesticated animal or human). The present sequence represents the  
CC complete cDNA sequence of a vector pCVTs, a DNA vector system for  
CC modifying the expression characteristics of an endogenous target gene  
CC within the genome of a eukaryotic cell comprising a 5' targeting  
CC construct and a 3' targeting construct, where the 5' and 3' targeting  
CC construct encode genetic elements required for RNA replication  
XX  
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 39.2%; Score 205.2; DB 5; Length 11282;  
Best Local Similarity 98.6%; Pred. No. 9.6e-61;  
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGTTAAAGATGAGTTAGCAACAT 320  
DB |||  
DB 664 ATCCAGTCTTATGCAATACTCTTGTAGTCTTGCACATGTTAAAGATGAGTTAGCAACAT 723  
QY 321 GCCTTACAGGACAGAAAACACCCGTGCATGCCGATTTGGTGAAGTAAAGTGTAGCAT 380  
DB |||  
DB 724 GCCTTACAGGACAGAAAACACCCGTGCATGCCGATTTGGTGAAGTAAAGTGTAGCAT 783  
QY 381 GTGCCTTATTAGGAGGACACAGCGGCTCTGACATGATTTGGACGACCACTAAATTC 440  
DB |||  
DB 784 GTGCCTTATTAGGAGGACACAGCGGCTCTGACATGATTTGGACGACCACTAAATTC 843  
QY 441 CGCATTCAGAGATATTTGATTTAAAGTGC 470  
DB |||  
DB 844 CGCATTCAGAGATATTTGATTTAAAGTGC 873

RESULT 73  
ABK10062  
ID ABK10062 standard; DNA; 5283 BP.  
XX  
AC ABK10062;  
XX  
XX  
DT 21-MAY-2002 (first entry)  
DE Expression vector construct pVGI.1 containing VEGF-2 insert.  
XX  
XX Human: vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;  
KW chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;  
KW allergic reaction; organ rejection; inflammatory condition; arrhythmia;  
KW hyperproliferative disorder; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cardiovascular disorder; embolism;  
KW heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.  
XX  
OS Synthetic.  
XX  
XX WO200211769-A1.  
FN  
PD 14-FEB-2002.  
XX  
XX 03-AUG-2001; 2001WO-US024658.  
PF  
XX 04-AUG-2000; 2000US-0223276P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Coleman TA;  
PI  
XX WPI; 2002-217153/27.  
DR  
XX Isolated nucleic acid having expression vector construct with vascular  
XX endothelial growth factor-2 insert, useful for treating chronic limb  
PT ischaemia or myocardial ischaemia, autoimmune disorders and allergic  
PT conditions.

XX Disclosure; Fig 31; 241pp; English.  
PS  
XX The invention relates to an isolated nucleic acid comprising pVGI.1  
CC expression vector construct containing the vascular endothelial growth  
CC factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host  
CC cell by transducing, transforming or transfecting a host cell with the  
CC DNA and for treating a patient having chronic limb ischaemia or  
CC myocardial ischaemia, or a disease or disorder selected from autoimmune  
CC disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or  
CC conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.  
CC Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),  
CC diseases due to viral, bacterial, fungal or parasitic infection,  
CC cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve  
CC diseases, aneurysms, arterial occlusive disorders and embolism. This  
CC sequence represents the pVGI.1 expression vector containing the VEGF-2  
CC insert  
XX  
SQ Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;

Query Match 35.9%; Score 187.6; DB 6; Length 5283;  
Best Local Similarity 91.5%; Pred. No. 1e-54;  
Matches 214; Conservative 0; Mismatches 9; Indels 11; Gaps 1;

QY 300 GTAACGATGATTAGCAACATGCCCTTACAGAGAGAGAAAAGCACCGTCATGCCGATTG 359  
DB |||  
DB 252 GTAACGATGATTAGCAACATGCCCTTACAGAGAGAGAAAAGCACCGTCATGCCGATTG 311  
QY 360 GTGGAGATTAAG-----GTGGTACGATCGCTTATTAGGAGGCAACAGACGG 408  
DB |||  
DB 312 GTGGAGATTAAGTGTGTATGATCGTGTATGATCGCTTATTAGGAGGCAACAGACGG 371  
QY 409 GTCTGACATCGATTGGACGAACCACTAAATTCGCAATTGCGAGATATTGTTAAGTG 468  
DB |||  
DB 372 GTCTAACACGGATTGGACGAACCACTGAATTCGCAATTGCGAGATATTGTTAAGTG 431  
QY 469 CCTACTCTGATACATAAAGCGCAATTCACCATTCACCATTCGTTGTCACCT 522  
DB |||  
DB 432 CCCAGCTCGATACATAAAGCGCAATTCGACCATTCACCATTCGTTGTCACCT 485

RESULT 74  
AAD53272  
ID AAD53272 standard; DNA; 4993 BP.  
XX  
AC AAD53272;  
XX  
DT 28-MAY-2003 (first entry)  
DE MESV2/EGFP/RSV retroviral vector DNA.  
XX  
XX Retroviral vector; congenital disease; cancer; Parkinson's disease;  
KW Alzheimer's disease; gene therapy; retroviral DNA; ds.  
XX  
OS Retrovirus.  
XX  
XX WO200294989-A2.  
FN  
PD 28-NOV-2002.  
XX  
XX 17-MAY-2002; 2002WO-US015816.  
PF  
XX 18-MAY-2001; 2001US-0292201P.  
PR  
XX 30-NOV-2001; 2001US-0334972P.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
PA  
XX Edelman GW, Owens G;  
PI  
XX WPI; 2003-140366/13.  
DR  
XX New retroviral vector plasmid for introducing expressible polynucleotides  
PT into cells, comprises a retrovirus long terminal repeat having U5, R and  
PT conditions.

PT U3 regions, a constitutive transport element, and a cloning site.  
 XX Claim 18; Col 95-97; 61pp; English.  
 XX The invention relates to novel retroviral vector plasmids for introducing  
 CC expressible polynucleotides into cells. The vectors comprise a retrovirus  
 CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive  
 CC transport element (CTE) and a cloning site. The retroviral vector plasmid  
 CC is useful in introducing an expressible polynucleotide into a cell such  
 CC as a neural stem cell and in treating or ameliorating a pathologic  
 CC condition in a subject such as a congenital diseases, cancer, Parkinson's  
 CC disease or Alzheimer's disease. The plasmid may also be used to produce  
 CC retroviral vectors useful for delivering genes into eukaryotic cells in  
 CC culture and in living organisms. Sequences of the invention are also  
 CC useful in gene therapy. The present sequence is MESV2/EGFP/RSV retroviral  
 CC vector DNA  
 XX  
 SQ Sequence 4993 BP; 1206 A; 1328 C; 1303 G; 1156 T; 0 U; 0 Other;  
 Query Match 33.5%; Score 175.2; DB 7; Length 4993;  
 Best Local Similarity 98.3%; Pred. No. 2.4e-50;  
 Matches 177; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 259 AAATGTAGTCTTATGCAATACCTTGTAGTCTTGTCAACATGTTAGGTAAC 318  
 DB 1907 AAATGTAGTCTTATGCAATACCTTGTAGTCTTGTCAACATGTTAGGTAAC 1966  
 QY 319 ATGCTTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTGGTGAAGTAAAGGTGTACG 378  
 DB 1967 ATGCTTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTGGTGAAGTAAAGGTGTACG 2026  
 QY 379 ATCGTGCTTATTAGGAAGGCAACAGACAGCGGTCTGACATGATTTGGACGACCACTAAAT 438  
 DB 2027 ATCGTGCTTATTAGGAAGGCAACAGACAGCGGTCTGACATGATTTGGACGACCACTAGAT 2086  
 RESULT 75  
 AAD53270  
 ID AAD53270 standard; DNA; 5643 BP.  
 AC AAD53270;  
 XX  
 DT 28-MAY-2003 (first entry)  
 DE MESVR/ACTE/IRESEGFP retroviral vector DNA.  
 XX  
 KW Retroviral vector; congenital disease; cancer; Parkinson's disease;  
 KW Alzheimer's disease; gene therapy; retroviral DNA; ds.  
 XX  
 OS Retrovirus.  
 XX  
 FN WO200294989-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 17-MAY-2002; 2002WO-US015816.  
 XX  
 PR 18-MAY-2001; 2001US-0292201P.  
 XX  
 PR 30-NOV-2001; 2001US-0334972P.  
 XX  
 PA (SCR ) SCRIPPS RES INST.  
 XX  
 XX Edelman GW, Owens G;  
 XX  
 XX WPI; 2003-140366/13.  
 XX  
 PT New retroviral vector plasmid for introducing expressible polynucleotides  
 PT into cells, comprises a retrovirus long terminal repeat having U5, R and  
 PT U3 regions, a constitutive transport element, and a cloning site.  
 XX  
 XX Claim 18; Col 88-91; 61pp; English.  
 XX  
 XX The invention relates to novel retroviral vector plasmids for introducing

CC expressible polynucleotides into cells. The vectors comprise a retrovirus  
 CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive  
 CC transport element (CTE) and a cloning site. The retroviral vector plasmid  
 CC is useful in introducing an expressible polynucleotide into a cell such  
 CC as a neural stem cell and in treating or ameliorating a pathologic  
 CC condition in a subject such as a congenital diseases, cancer, Parkinson's  
 CC disease or Alzheimer's disease. The plasmid may also be used to produce  
 CC retroviral vectors useful for delivering genes into eukaryotic cells in  
 CC culture and in living organisms. Sequences of the invention are also  
 CC useful in gene therapy. The present sequence is MESVR/ACTE/IRESEGFP  
 CC retroviral vector DNA  
 XX  
 SQ Sequence 5643 BP; 1356 A; 1505 C; 1472 G; 1310 T; 0 U; 0 Other;  
 Query Match 33.5%; Score 175.2; DB 7; Length 5643;  
 Best Local Similarity 98.3%; Pred. No. 2.5e-50;  
 Matches 177; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 259 AAATGTAGTCTTATGCAATACCTTGTAGTCTTGTCAACATGTTAGGTAAC 318  
 DB 2557 AAATGTAGTCTTATGCAATACCTTGTAGTCTTGTCAACATGTTAGGTAAC 2616  
 QY 319 ATGCTTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTGGTGAAGTAAAGGTGTACG 378  
 DB 2617 ATGCTTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTGGTGAAGTAAAGGTGTACG 2676  
 QY 379 ATCGTGCTTATTAGGAAGGCAACAGACAGCGGTCTGACATGATTTGGACGACCACTAAAT 438  
 DB 2677 ATCGTGCTTATTAGGAAGGCAACAGACAGCGGTCTGACATGATTTGGACGACCACTAGAT 2736

Search completed: March 11, 2004, 08:23:00  
 Job time : 463.959 secs





## ALIGNMENTS

RESULT 1  
 US-08-564-313-1  
 ; Sequence 1, Application US/08564313  
 ; Patent No. 5910488  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nabel, Elizabeth  
 ; APPLICANT: Nabel, Gary  
 ; APPLICANT: Lew, Denise  
 ; APPLICANT: Marquet, Magda  
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear  
 ; STREET: 620 Newport Center Drive 16th Floor  
 ; CITY: Newport Beach  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/564,313  
 ; FILING DATE: 01-DEC-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/074,344  
 ; FILING DATE: 07-JUN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israel, Ned  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: VICAL.033CP1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4965 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: circular  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHEetical: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE:  
 ; IMMEDIATE SOURCE:  
 ; CLONE: HLA-B7 and Beta-2

US-08-564-313-1  
 Query Match 98.5%; Score 515; DB 2; Length 4965;  
 Best Local Similarity 99.0%; Pred. No. 3.9e-174;  
 Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGTTGTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAGCTACA 60  
 Db 1 CTGCTCCCTGTTGTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAGCTACA 60  
 QY 61 ACAAGGCAAGCTTGACCCACAAATTCATGAATCTGCTTAGGGTTAGGGGTTTGGC 120  
 Db 61 ACAAGGCAAGCTTGACCCACAAATTCATGAATCTGCTTAGGGTTAGGGGTTTGGC 120  
 QY 121 CTGCTCCGATGTAGGGCCAGATATTTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 121 CTGCTCCGATGTAGGGCCAGATATTTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180

QY 181 CGAAAAGCGGGCTTCGGTTGTACGCGGTTAGAGTCCCTCAGGATATAGTAGTTGCG 240  
 Db 181 CGAAAAGCGGGCTTCGGTTGTACGCGGTTAGAGTCCCTCAGGATATAGTAGTTGCG 240  
 QY 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 300  
 Db 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 300  
 QY 301 TAAAGTGTAGTGTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTGG 360  
 Db 301 TAAAGTGTAGTGTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTGG 360  
 QY 361 TGGAGTAAAGTGTGTACGATCGTCCCTTATTAGGAAGCAACAGAGCGGTCTGACATGGA 420  
 Db 361 TGGAGTAAAGTGTGTACGATCGTCCCTTATTAGGAAGCAACAGAGCGGTCTGACATGGA 420  
 QY 421 TTGGACGAACCACTAAATTCGGATTTCAGAGATATTGTTAAGTGGCTAGCTCGATA 480  
 Db 421 TTGGACGAACCACTAAATTCGGATTTCAGAGATATTGTTAAGTGGCTAGCTCGATA 480  
 QY 481 CAATTAAGCGCAATTGACCAATTCACCAATTGGTGTGCACCTC 523  
 Db 481 CTCATAGAGCCATTGACCAATTCACCAATTGGTGTGCACCTC 523  
 RESULT 2  
 PCT-US94-06069-1  
 ; Sequence 1, Application PC/TUS9406069  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vical Incorporated  
 ; APPLICANT: Regents of the University of Michigan  
 ; APPLICANT: Nabel, Elizabeth  
 ; APPLICANT: Nabel, Gary  
 ; APPLICANT: Lew, Denise  
 ; APPLICANT: Marquet, Magda  
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear  
 ; STREET: 620 Newport Center Drive 16th Floor  
 ; CITY: Newport Beach  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/06069  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/074,344  
 ; FILING DATE: 07-JUN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israel, Ned  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: VICAL.033VPC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4965 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: circular  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHEtical: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE:  
 ; IMMEDIATE SOURCE:  
 ; CLONE: HLA-B7 and Beta-2

FRAGMENT TYPE:  
ORIGINAL SOURCE:  
STRAIN: HLA-B7 and Beta-2  
PCT-US94-06069-1

Query Match 98.5%; Score 515; DB 5; Length 4965;  
Best Local Similarity 99.0%; Pred. No. 3.9e-174;  
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60  
DB 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60

QY 61 ACAAGCAAGGCTTACCGCAAAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 120  
DB 61 ACAAGCAAGGCTTACCGCAAAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 120

QY 121 CTGCTTCGGGATGTACGGGCGAGATATCGGCTATCTGAGGGGACTAGGGGTGTGTAGG 180  
DB 121 CTGCTTCGGGATGTACGGGCGAGATATCGGCTATCTGAGGGGACTAGGGGTGTGTAGG 180

QY 181 CGAAAAGCGGGCTTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
DB 181 CGAAAAGCGGGCTTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240

QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300

QY 301 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGCGATTGG 360  
DB 301 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGCGATTGG 360

QY 361 TGGAGTAAAGTGTGTAGTGTGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420  
DB 361 TGGAGTAAAGTGTGTAGTGTGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420

QY 421 TTGAGCAACACTTAATTCGGATTCGAGATATGATTTAAGTCCCTAGCTCGATA 480  
DB 421 TTGAGCAACACTTAATTCGGATTCGAGATATGATTTAAGTCCCTAGCTCGATA 480

QY 481 CAATAAAGCCATTGTGACCAATCAACATTTGGTGCACCTC 523  
DB 481 CTCTAGACCCATTGTGACCAATCAACATTTGGTGCACCTC 523

RESULT 3  
US-08-564-313-2/c  
Sequence 2, Application US/08564313  
Patent No. 5910488

GENERAL INFORMATION:  
APPLICANT: Nabel, Elizabeth  
APPLICANT: Nabel, Gary  
APPLICANT: Lew, Denise  
APPLICANT: Marquet, Magda  
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/564,313  
FILING DATE: 01-DEC-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/074,344  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: VICAL.033CP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4059 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
IMMEDIATE SOURCE:  
CLONE: HLA-B7  
US-08-564-313-2

Query Match 96.7%; Score 505.6; DB 2; Length 4059;  
Best Local Similarity 99.0%; Pred. No. 8.2e-171;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60  
DB 3415 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 3356

QY 61 ACAAGCAAGGCTTACCGCAAAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 120  
DB 3355 ACAAGCAAGGCTTACCGCAAAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 3296

QY 121 CTGCTTCGGGATGTACGGGCGAGATATCGGCTATCTGAGGGGACTAGGGGTGTGTAGG 180  
DB 3295 CTGCTTCGGGATGTACGGGCGAGATATCGGCTATCTGAGGGGACTAGGGGTGTGTAGG 3236

QY 181 CGAAAAGCGGGCTTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
DB 3235 CGAAAAGCGGGCTTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 3176

QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 3175 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 3116

QY 301 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGCTCGATGG 360  
DB 3115 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGCTCGATGG 3056

QY 361 TGGAGTAAAGTGTGTAGTGTGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420  
DB 3055 TGGAGTAAAGTGTGTAGTGTGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 2996

QY 421 TTGAGCAACACTTAATTCGGATTCGAGATATGATTTAAGTCCCTAGCTCGATA 479  
DB 2995 TTGAGCAACACTTAATTCGGATTCGAGATATGATTTAAGTCCCTAGCTCGATA 2936

QY 480 ACAATAAAGCCATTGTGACCAATCAACATTTGGTGTGCACCTC 523  
DB 2935 ACAATAAAGCCATTGTGACCAATCAACATTTGGTGTGCACCTC 2892

RESULT 4  
PCT-US94-06069-2/c  
Sequence 2, Application PC/TUS9406069  
GENERAL INFORMATION:  
APPLICANT: Nabel, Elizabeth  
APPLICANT: Regente of the University of Michigan  
APPLICANT: Nabel, Elizabeth

23

23

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Db 261 CAAAAAGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 320
QY 241 TTTTGCATAGGAGGGGAAATGCTCTTATGCAATCTTGTAGTCTTGCACATGG 300
Db 321 TTTTGCATAGGAGGGGAAATGCTCTTATGCAATCTTGTAGTCTTGCACATGG 380
QY 301 TAAGATGAGTTAGCAATGCTCTTACAGGAGAGAAAAAGCACCGTGTGATGCGATTGG 360
Db 381 TAAGATGAGTTAGCAATGCTCTTACAGGAGAGAAAAAGCACCGTGTGATGCGATTGG 440
QY 361 TGGAGTAAAGTTAGCAATGCTCTTATGCAATCTTGTAGTCTTGCACATGG 420
Db 441 TGGAGTAAAGTTAGCAATGCTCTTATGCAATCTTGTAGTCTTGCACATGG 500
QY 421 TTGAGCAACCACTAAATTCGATTCGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479
Db 501 TTGAGCAACCACTAAATTCGATTCGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 560
QY 480 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 523
Db 561 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 604

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RESULT 6

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US-08-235-277-1
; Sequence 1, Application US/08235277
; Patent No. 5733543
; GENERAL INFORMATION:
; APPLICANT: NABEL, GARY J
; APPLICANT: WOFFENDIN, CLIVE
; APPLICANT: YANG, NIN-SUN
; APPLICANT: SHEEHY, MICHAEL J
; TITLE OF INVENTION: INTRODUCTION OF HIV-PROTECTIVE GENES
; TITLE OF INVENTION: INTO CELLS BY PARTICLE-MEDIATED GENE TRANSFER
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,277
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5733543man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 6042-008-68
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Other nucleic acid

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US-08-235-277-1
Query Match 96.7%; Score 505.6; DB 1; Length 5653;
Best Local Similarity 99.0%; Pred. No. 9,8e-171;
Matches 519; Conservative 0; Mismatches 4; Indels 1;

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QY 1 CTGCTCCCTGCTTGTGTGCTGAGTGTAGTGTGCGGCGGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTTGTGTGCTGAGTGTAGTGTGCGGCGGCAAAATTTAAGCTACA 140
QY 61 ACAAGGCAAGGCTTGACCGACAATTCATCAAGAATCTGCTTAGGGTTAGGGGTTTGG 120
Db 141 ACAAGGCAAGGCTTGACCGACAATTCATCAAGAATCTGCTTAGGGTTAGGGGTTTGG 200
QY 121 CTGCTTCGCGATGTAGGCGCCAGATATTGCGGTATCTGAGGGGACTAGGGTGTGTTAG 180
Db 201 CTGCTTCGCGATGTAGGCGCCAGATATTGCGGTATCTGAGGGGACTAGGGTGTGTTAG 260
QY 181 CGAAAAGCGGGGCTTCGCTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCGC 240
Db 261 CGAAAAGCGGGGCTTCGCTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCGC 320
QY 241 TTTTGCATAGGAGGGGAAATGAGTGTCTTATGCAATCTTGTAGTCTTGCACATGG 300
Db 321 TTTTGCATAGGAGGGGAAATGAGTGTCTTATGCAATCTTGTAGTCTTGCACATGG 380
QY 301 TAAAGTAAAGTTAGCAATGCTCTTACAGGAGAGAAAAAGCACCGTGTGATGCGATTGG 360
Db 381 TAAAGTAAAGTTAGCAATGCTCTTACAGGAGAGAAAAAGCACCGTGTGATGCGATTGG 440
QY 361 TGGAGTAAAGTTAGCAATGCTCTTATGCAATCTTGTAGTCTTGCACATGG 420
Db 441 TGGAGTAAAGTTAGCAATGCTCTTATGCAATCTTGTAGTCTTGCACATGG 500
QY 421 TTGAGCAACCACTAAATTCGATTCGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479
Db 501 TTGAGCAACCACTAAATTCGATTCGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 560
QY 480 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 523
Db 561 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 604

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RESULT 7

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US-08-462-859A-6
; Sequence 6, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 6:

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SEQUENCE CHARACTERISTICS:  
LENGTH: 8591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393..3668  
US-08-462-859A-6

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 120  
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 4835  
QY 121 CTGCTTCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 180  
DB 4836 CTGCTTCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 4895  
QY 181 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240  
DB 4896 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 4955  
QY 241 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 5136 TTTGACGACCACTGAAATTCGCAATTCAGAGATATTTAAGTGCCTAGCTCGAT 5195  
QY 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
DB 5196 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 5239

## RESULT 8

US-08-462-859A-6  
Sequence 6, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.  
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barthard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393..3668  
US-08-462-859A-8

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 120  
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 4835  
QY 121 CTGCTTCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 180  
DB 4836 CTGCTTCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 4895  
QY 181 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240  
DB 4896 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 4955  
QY 241 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 4956 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015  
QY 301 TTAACGATGATGACCAATTCGCAATTCAGAGATATTTAAGTGCCTAGCTCGAT 360  
DB 5016 TTAACGATGATGACCAATTCGCAATTCAGAGATATTTAAGTGCCTAGCTCGAT 5075  
QY 361 TGAAGTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 5076 TGAAGTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5135  
QY 421 TFGAGCAACCACTAAATTCGCAATTCAGAGATATTTAAGTGCCTAGCTCGAT 479  
DB 5136 TFGAGCAACCACTAAATTCGCAATTCAGAGATATTTAAGTGCCTAGCTCGAT 5195  
QY 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
DB 5196 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 5239

## RESULT 9

US-08-123-659A-6  
Sequence 6, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.

;; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
;; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
;; TITLE OF INVENTION: of B-Amyloid Peptide  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: Anne Rosenblum  
;; STREET: 163 Delaware Avenue, Suite 212  
;; CITY: Delmar  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 12054  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/123,659A  
;; FILING DATE: 20-SEP-1993  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Rosenblum, Anne M.  
;; REGISTRATION NUMBER: 30,419  
;; REFERENCE/DOCKET NUMBER: 31,844-01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (518)475-0611  
;; TELEFAX: (518)475-0619  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8591 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: circular  
;; MOLECULE TYPE: cDNA  
;; FEATURES:  
;; NAME/KEY: CDS  
;; LOCATION: 2393..3868  
US-08-123-659A-6

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAAGTACA 60  
Db 4716 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAAGTACA 4775  
Qy 61 ACAAGGCAAGGCTTGCACCAATTCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGCG 120  
Db 4776 ACAAGGCAAGGCTTGCACCAATTCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGCG 4835  
Qy 121 CTGCTTCGGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTTAGG 180  
Db 4836 CTGCTTCGGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTTAGG 4895  
Qy 181 CGAAAACGGGGCTTCGGTTGTAGCGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
Db 4896 CGAAAACGGGGCTTCGGTTGTAGCGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 4955

Db 5136 TTGGAGCAACCACTGAATTCGCAATTCGAGAGATAATTTAAAGTCCCTAGCTCGAT 5195  
Qy 480 ACAATRAAGCCATTGACCAATTCACCAATTTGGTGGCACTC 523  
Db 5196 ACAATAAAGCCATTGACCAATTCACCAATTTGGTGGCACTC 5239

RESULT 10  
US-08-123-659A-8  
;; Sequence 8, Application US/08123659A  
;; Patent No. 5656477  
;; GENERAL INFORMATION:  
;; APPLICANT: Jacobsen, J. S.  
;; APPLICANT: Vittek, M. P.  
;; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
;; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
;; TITLE OF INVENTION: of B-Amyloid Peptide  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Anne Rosenblum  
;; STREET: 163 Delaware Avenue, Suite 212  
;; CITY: Delmar  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 12054  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/123,659A  
;; FILING DATE: 20-SEP-1993  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Rosenblum, Anne M.  
;; REGISTRATION NUMBER: 30,419  
;; REFERENCE/DOCKET NUMBER: 31,844-01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (518)475-0611  
;; TELEFAX: (518)475-0619  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8591 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: circular  
;; MOLECULE TYPE: cDNA  
;; FEATURES:  
;; NAME/KEY: CDS  
;; LOCATION: 2393..3853  
US-08-123-659A-8

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAAGTACA 60  
Db 4716 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAAGTACA 4775  
Qy 61 ACAAGGCAAGGCTTGCACCAATTCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGCG 120  
Db 4776 ACAAGGCAAGGCTTGCACCAATTCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGCG 4835  
Qy 121 CTGCTTCGGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTTAGG 180  
Db 4836 CTGCTTCGGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTTAGG 4895  
Qy 181 CGAAAACGGGGCTTCGGTTGTAGCGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
Db 4896 CGAAAACGGGGCTTCGGTTGTAGCGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 4955

QY 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATACCTCTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATACCTCTGTAGTCTTGCACATGG 5015  
QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAACACCGTGCATGCCATGG 360  
Db 5016 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAACACCGTGCATGCCATGG 5075  
QY 361 TGGAGTAAAGTGTGATGATGCTTATAGGAAGCAACAGAGCGGTCTGCATGGA 420  
Db 5076 TGGAGTAAAGTGTGATGCTTATAGGAAGCAACAGAGCGGTCTGCATGGA 5135  
QY 421 TTGGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 479  
Db 5136 TTGGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 5195  
QY 480 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 523  
Db 5196 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 5239

## RESULT 11

US-08-464-247A-6  
; Sequence 6, Application US/08464247A  
; Patent No. 5693478  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,247A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-683-2158  
; TELEFAX: 201-683-4117  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8591 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2393..3868  
US-08-464-247A-6

Query Match 36.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 59.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGAGTGGCTGCTGAGTGGAGGAGCAAAATTTAAGCTACA 60  
|||||

Db 4716 CTGCTCCCTGCTGTGTGAGTGGCTGCTGAGTGGAGGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAGGCAAGCTGTGACCCACAAATTTGCATCAAGAACTGCTTAGGTTAGGCGTTTTCGG 120  
Db 4776 ACAGGCAAGCTGTGACCCACAAATTTGCATCAAGAACTGCTTAGGTTAGGCGTTTTCGG 4835  
QY 121 CTGCTTCGCGATGTACGGCCAGATATTCGCGTATCTCAGGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGTACGGCCAGATATTCGCGTATCTCAGGGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAGCGGGGCTTCGGTTTTCGCGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 4896 CGAAAGCGGGGCTTCGGTTTTCGCGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 4955  
QY 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATACCTCTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATACCTCTGTAGTCTTGCACATGG 5015  
QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAACACCGTGCATGCCATGG 360  
Db 5016 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAACACCGTGCATGCCATGG 5075  
QY 361 TGGAGTAAAGTGTGATGATGCTTATAGGAAGCAACAGAGCGGTCTGCATGGA 420  
Db 5076 TGGAGTAAAGTGTGATGCTTATAGGAAGCAACAGAGCGGTCTGCATGGA 5135  
QY 421 TTGGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 479  
Db 5136 TTGGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 5195  
QY 480 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 523  
Db 5196 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 5239

## RESULT 12

US-08-464-247A-8  
; Sequence 8, Application US/08464247A  
; Patent No. 5693478  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,247A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-683-2158  
; TELEFAX: 201-683-4117  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8591 base pairs  
; TYPE: nucleic acid



STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393...3853  
US-08-464-248A-8

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 60  
Db 4716 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 4775  
QY 61 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 120  
Db 4776 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 4835  
QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAACGGGGCTTCGCTGCTGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 240  
Db 4896 CGAAAACGGGGCTTCGCTGCTGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 4955  
QY 241 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 5015  
QY 301 TACGATGATGTAGCAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 360  
Db 5016 TACGATGATGTAGCAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 5075  
QY 361 TGGAGTAGGTCGTAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 420  
Db 5076 TGGAGTAGGTCGTAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 5135  
QY 421 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTAATTAAGTCCCTAGCTCCAT 479  
Db 5136 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTAATTAAGTCCCTAGCTCCAT 5195  
QY 480 ACAATAAGCCCATTTGACCAATTCACCAATTTGTCACCTC 523  
Db 5196 ACAATAAGCCCATTTGACCAATTCACCAATTTGTCACCTC 5239

RESULT 13  
US-08-464-248A-6  
Sequence 6, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393...3868  
US-08-464-248A-5

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 60  
Db 4716 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 4775  
QY 61 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 120  
Db 4776 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 4835  
QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAACGGGGCTTCGCTGCTGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 240  
Db 4896 CGAAAACGGGGCTTCGCTGCTGAGGTCGCTGAGTAGTGGCGAGCAAAAATTTAAGTACA 4955  
QY 241 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 5015  
QY 301 TACGATGATGTAGCAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 360  
Db 5016 TACGATGATGTAGCAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 5075  
QY 361 TGGAGTAGGTCGTAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 420  
Db 5076 TGGAGTAGGTCGTAACATGCTTCAAGGAGAGAAAAGCAACGCTGATCCCGATTGG 5135  
QY 421 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTAATTAAGTCCCTAGCTCCAT 479  
Db 5136 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTAATTAAGTCCCTAGCTCCAT 5195  
QY 480 ACAATAAGCCCATTTGACCAATTCACCAATTTGTCACCTC 523  
Db 5196 ACAATAAGCCCATTTGACCAATTCACCAATTTGTCACCTC 5239

RESULT 14  
US-08-464-248A-8  
Sequence 8, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393..3853  
US-08-464-248A-8

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTCTGTGTGTGGAGGTGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTCTGTGTGTGGAGGTGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAAGGCAAGCTTGACCGCAATTTGCAATGAAGATCTGCTTAGGGTTAGGGCTTTTCG 120  
DB 4776 ACAAGGCAAGCTTGACCGCAATTTGCAATGAAGATCTGCTTAGGGTTAGGGCTTTTCG 4835  
QY 121 CTGCTTCGATGATCGGCGCCAGATATTGCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 4836 CTGCTTCGATGATCGGCGCCAGATATTGCGGTATCTGAGGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAAGCGGGGCTTGGTTAGCGGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 240  
DB 4896 CGAAAAGCGGGGCTTGGTTAGCGGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 4955  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 4956 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015  
QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 360  
DB 5016 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 5075  
QY 361 TGGAGTAAAGTGGTAGCATGTCGCTTATTAGGAAGCAACAGACCGCTGCATGCAATGGA 420  
DB 5076 TGGAGTAAAGTGGTAGCATGTCGCTTATTAGGAAGCAACAGACCGCTGCATGCAATGGA 5135  
QY 421 TTGGACCAACCACTAAATTCGGATTTCAGAGAT-ATTGTTATTAAAGTCCCTAGCTCGAT 479  
DB 5136 TTGGACCAACCACTAAATTCGGATTTCAGAGAT-ATTGTTATTAAAGTCCCTAGCTCGAT 5195  
QY 480 ACAATAAAGCCCAATTGACCAATTCCACCAATTGGTGTGCACCTC 523

DB 5196 ACAATAAAGCCCAATTGACCAATTCCACCAATTGGTGTGCACCTC 5239  
RESULT 15  
US-09-479-122-18  
Sequence 18, Application US/09479122  
Patent No. 6410266  
GENERAL INFORMATION:  
APPLICANT: HARRINGTON, JOHN J.  
APPLICANT: SHERF, BRUCE  
APPLICANT: RUNDLETT, STEPHEN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
FILE OF INVENTION: ENDOGENOUS GENES  
FILE REFERENCE: 0221-0003C  
CURRENT APPLICATION NUMBER: US/09/479,122  
CURRENT FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: 09/276,820  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 09/159,643  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 08/941,223  
PRIOR FILING DATE: 1997-09-26  
PRIOR APPLICATION NUMBER: 09/263,814  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: 09/253,022  
PRIOR FILING DATE: 1999-02-19  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 18  
LENGTH: 6836  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-479-122-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTCTGTGTGTGGAGGTGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACA 60  
DB 1299 CTGCTCCCTCTGTGTGTGGAGGTGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACA 1358  
QY 61 ACAAGGCAAGCTTGACCGCAATTTGCAATGAAGATCTGCTTAGGGTTAGGGCTTTTCG 120  
DB 1359 ACAAGGCAAGCTTGACCGCAATTTGCAATGAAGATCTGCTTAGGGTTAGGGCTTTTCG 1418  
QY 121 CTGCTTCGATGATCGGCGCCAGATATTGCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 1419 CTGCTTCGATGATCGGCGCCAGATATTGCGGTATCTGAGGGGACTAGGGTGTGTTAGG 1478  
QY 181 CGAAAAGCGGGGCTTGGTTAGCGGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 240  
DB 1479 CGCCCAGCGGGGCTTGGTTAGCGGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 1538  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 1539 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598  
QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 360  
DB 1599 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 1658  
QY 361 TGGAGTAAAGTGGTAGCATGTCGCTTATTAGGAAGCAACAGACCGCTGCATGCAATGGA 420  
DB 1659 TGGAGTAAAGTGGTAGCATGTCGCTTATTAGGAAGCAACAGACCGCTGCATGCAATGGA 1718  
QY 421 TTGGACCAACCACTAAATTCGGATTTCAGAGAT-ATTGTTATTAAAGTCCCTAGCTCGAT 479  
DB 1719 TTGGACCAACCACTAAATTCGGATTTCAGAGAT-ATTGTTATTAAAGTCCCTAGCTCGAT 1778  
QY 480 ACAATAAAGCCCAATTGACCAATTCCACCAATTGGTGTGCACCTC 523

D6 1779 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822

## RESULT 16

US-09-484-997-18  
; Sequence 16, Application US/09484997  
; Patent No. 6524918  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003J  
; CURRENT APPLICATION NUMBER: US/09/484,997  
; CURRENT FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-484-997-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
DB 1299 CTGCTCCCTGCTTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1358  
QY 61 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 120  
DB 1359 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 1418  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 1419 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 1478  
QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTGCG 240  
DB 1479 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTGCG 1538  
QY 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 1539 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598  
QY 301 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
DB 1599 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1658  
QY 361 TGGAGTAAAGTGTGATGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420  
DB 1659 TGGAGTAAAGTGTGATGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1718  
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
DB 1719 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1778  
QY 480 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
DB 1779 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822

## RESULT 17

US-09-481-355-18  
; Sequence 18, Application US/09481355  
; Patent No. 6524824  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003F  
; CURRENT APPLICATION NUMBER: US/09/481,355  
; CURRENT FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-481-355-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
DB 1299 CTGCTCCCTGCTTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1358  
QY 61 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 120  
DB 1359 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 1418  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 1419 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 1478  
QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTGCG 240  
DB 1479 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTGCG 1538  
QY 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 1539 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598  
QY 301 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
DB 1599 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1658  
QY 361 TGGAGTAAAGTGTGATGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420  
DB 1659 TGGAGTAAAGTGTGATGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1718  
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
DB 1719 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1778  
QY 480 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
DB 1779 ACAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822



Patent No. 6623958  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003H  
; CURRENT APPLICATION NUMBER: US/09/484,996  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1998-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-484-996-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 1358

QY 61 ACAAGCAGAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGCGGTTTGGG 120  
Db 1359 ACAAGCAGAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGCGGTTTGGG 1418

QY 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 1419 CTGCTTCGGGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 1478

QY 181 CGAAAACGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 1479 CGCCACGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 1538

QY 241 TTTTGATAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 1539 TTTTGATAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598

QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
Db 1599 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1658

QY 361 TGGAGTAGAGTGTGACGATGCTTATAGGAGGCAACAGAGCGGTCTGACATGGA 420  
Db 1659 TGGAGTAGAGTGTGACGATGCTTATAGGAGGCAACAGAGCGGTCTGACATGGA 1718

QY 421 TTGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1719 TTGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1778

QY 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
Db 1779 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 1822

RESULT 21  
US-09-479-123-18  
; Sequence 18, Application US/09479123  
; Patent No. 6670185

; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003B  
; CURRENT APPLICATION NUMBER: US/09/479,123  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-479-123-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 1358

QY 61 ACAAGCAGAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGCGGTTTGGG 120  
Db 1359 ACAAGCAGAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGCGGTTTGGG 1418

QY 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 1419 CTGCTTCGGGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 1478

QY 181 CGAAAACGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 1479 CGCCACGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 1538

QY 241 TTTTGATAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 1539 TTTTGATAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598

QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
Db 1599 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1658

QY 361 TGGAGTAGAGTGTGACGATGCTTATAGGAGGCAACAGAGCGGTCTGACATGGA 420  
Db 1659 TGGAGTAGAGTGTGACGATGCTTATAGGAGGCAACAGAGCGGTCTGACATGGA 1718

QY 421 TTGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1719 TTGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1778

QY 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
Db 1779 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 1822

RESULT 22  
US-09-479-122-22  
; Sequence 22, Application US/09479122  
; Patent No. 6410266  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE



QY 480 ACAATAAGCCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 1675

## RESULT 24

US-09-479-122-28  
; Sequence 28, Application US/09479122  
; Patent No. 6410266  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERP, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; FILE REFERENCE: 0221-0003C  
; CURRENT APPLICATION NUMBER: US/09/479,122  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 9737  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8347)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; NAME/KEY: modified\_base  
; LOCATION: (8499)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-479-122-28

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTAGTGCAGGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTAGTGCAGGCAAAATTTAAGCTACA 1211  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTTAGGGTTAGCGTTTTCG 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTTAGGGTTAGCGTTTTCG 1271  
QY 121 CTGCTCCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGGTGTTCG 180  
Db 1272 CTGCTCCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGGTGTTCG 1331  
QY 181 CGAAAAGCGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCG 240  
Db 1332 CGCCAGCGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCG 1391  
QY 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGG 1451  
QY 301 TAACGATGATGATGACATCGCTCTTACAGGAGAGAAAGCAACCGTGCATGCGGATTGG 360  
Db 1452 TAACGATGATGATGACATCGCTCTTACAGGAGAGAAAGCAACCGTGCATGCGGATTGG 1511  
QY 361 TGGAGTAAAGTGTGATGATCGTCTTATAGGAGGCAACAGACGGGCTCAGCATGGA 420

Db 1512 TGGAGTAAAGTGTGATGATCGTCTTATAGGAGGCAACAGACAGGTCTGACATGGA 1571  
QY 421 TTGACGCAAGCACTAAATTCGGATTCGAGAGAT-ATTGTATTATTAAGTCCCTAGTGGAT 479  
Db 1572 TTGACGCAAGCACTAAATTCGGATTCGAGAGATTAATTGTATTATTAAGTCCCTAGTGGAT 1631  
QY 480 ACAATAAGCCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 1675

## RESULT 25

US-09-484-997-22  
; Sequence 22, Application US/09484997  
; Patent No. 6524818  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERP, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; FILE REFERENCE: 0221-0003J  
; CURRENT APPLICATION NUMBER: US/09/484,997  
; CURRENT FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 9737  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8347)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; NAME/KEY: modified\_base  
; LOCATION: (8499)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-484-997-22

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTAGTGCAGGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTAGTGCAGGCAAAATTTAAGCTACA 1211  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTTAGGGTTAGCGTTTTCG 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTTAGGGTTAGCGTTTTCG 1271  
QY 121 CTGCTCCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGGTGTTCG 180  
Db 1272 CTGCTCCGCGATGACGGGCGAGATTCGCGTATCTGAGGGGACTAGGGTGTTCG 1331  
QY 181 CGAAAAGCGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCG 240  
Db 1332 CGCCAGCGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCG 1391  
QY 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGG 1451

RESULT 26

RESULT 27

US-09-484-997-28  
; sequence 28. Application US/09484997

; FACEID NO. 6324818  
; GENERAL INFORMATION:

Db	1152	CTGCTCCCTGCTGTGTGTGTGAGTGCTGTAGTAGTGGCGAGCAAAATTTAAGCTAC	1211
Qy	61	ACAGGCAAGGCTTGACCGACAATTCATGATGAAGAAATCTGCTTAGGCTTAGCCGTTTGGC	120
Db	1212	ACAGGCAAGGCTTGACCGACAATTCATGATGAAGAAATCTGCTTAGGCTTAGCCGTTTGGC	1271
Qy	121	CTGCTTCGCGATGTACGGCCAGATATTTGCGCTATCTGAGGGACCTAGGGTGTATTAGG	180
Db	1272	CTGCTTCGCGATGTACGGCCAGATATTCAGCGTATCTGAGGGACCTAGGGTGTATTAGG	1331
Qy	181	CGAAAAGCGGGGCTTCGGTTGTACGGGTTAGGACTCCCTCAGGATATAGTAGTTTCCG	240

Query Match	95.8%	Score 500.8;	DB 4;	Length 9737;
Best Local Similarity	98.5%;	Pred. No. 7.1e-169;		
Matches 516;	Conservative	0;	Mismatches 7;	Indels 1; Gaps 1;

	Query Match	95.8%	Score 500.8	DB 4	Length 9737
	Best Local Similarity	98.5%	Pred. No. 7.1e-169		
	Matches 516	Conservative 0	Mismatches 7	Indels 1	Gaps 1
Qy	1	CTGCTCCCTGCTTGTGTTGGAGGTGCGTGTAGTGTGCGCGAGCAAAATTTAAGTACA	60		
Db	1152	CTGCTCCCTGCTTGTGTTGGAGTGTGCTGTAGTGTGCGCGAGCAAAATTTAAGTACA	1211		
Qy	61	ACAAGCGAAGGCTTGACCGACAATTCGATCAGTAAGATCTGCTTAGGCTTTAGCGCTTTTGG	120		
Db	1212	ACAAGCGAAGGCTTGACCGACAATTCGATCAGTAAGATCTGCTTAGGCTTTAGCGCTTTTGG	1271		



121 CTGCTTCCGATGTAACGGCCAGATATTCGGTATCTCAGGGGACTAGGGTGTGTTTAGG 180  
 1272 CTGCTTCCGATGTAACGGCCAGATATTCGGTATCTCAGGGGACTAGGGTGTGTTTAGG 1331  
 181 CGAAAGCGGGGCTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
 1332 CGCCAGCGGGGCTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 1391  
 241 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATACTCTTTGAGTCTTGCAACATGG 300  
 1392 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATACTCTTTGAGTCTTGCAACATGG 1451  
 301 TAACGATGATGACATGCTTCAAGGAGGAAAGACCGTGCATGCCGATTCG 360  
 1452 TAACGATGATGACATGCTTCAAGGAGGAAAGACCGTGCATGCCGATTCG 1511  
 361 TGGAGTATAGGTTGACGATCGCTTATGAGGAGGAAAGACCGTGCATGCCGATTCG 420  
 1512 TGGAGTATAGGTTGACGATCGCTTATGAGGAGGAAAGACCGTGCATGCCGATTCG 1571  
 421 TTGACGAACCACTAAATTCGGCATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
 1572 TTGACGAACCACTAAATTCGGCATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631  
 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
 1632 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 1675

RESULT 28  
 US-09-481-355-22  
 ; Sequence 22, Application US/09481355  
 ; Patent No. 6524824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003F  
 ; CURRENT APPLICATION NUMBER: US/09/481,355  
 ; PRIOR FILING DATE: 2000-01-12  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR FILING DATE: 1997-09-26  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-481-355-22

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTGTGTTGGAGGTCGCTAGTAGGCGAGCAAAATTTAAGCTACA 60

1152 CTGCTCCCTGCTGTGTTGGAGGTCGCTAGTAGTGGCGAGCAAAATTTAAGCTACA 1211  
 61 ACAAGGCAAGGCTTGACCGCAAAATTCGATGCAAGAAATCTGCTAGGCTTAGGGCTTTTCGG 120  
 1212 ACAAGGCAAGGCTTGACCGCAAAATTCGATGCAAGAAATCTGCTAGGCTTAGGGCTTTTCGG 1271  
 121 CTGCTTCCGATGTAACGGCCAGATATTCGGTATCTCAGGGGACTAGGGTGTGTTTAGG 180  
 1272 CTGCTTCCGATGTAACGGCCAGATATTCGGTATCTCAGGGGACTAGGGTGTGTTTAGG 1331  
 181 CGAAAGCGGGGCTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
 1332 CGCCAGCGGGGCTTCGGTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 1391  
 241 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATACTCTTTGAGTCTTGCAACATGG 300  
 1392 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATACTCTTTGAGTCTTGCAACATGG 1451  
 301 TAACGATGATGACATGCTTCAAGGAGGAAAGACCGTGCATGCCGATTCG 360  
 1452 TAACGATGATGACATGCTTCAAGGAGGAAAGACCGTGCATGCCGATTCG 1511  
 361 TGGAGTATAGGTTGACGATCGCTTATGAGGAGGAAAGACCGTGCATGCCGATTCG 420  
 1512 TGGAGTATAGGTTGACGATCGCTTATGAGGAGGAAAGACCGTGCATGCCGATTCG 1571  
 421 TTGACGAACCACTAAATTCGGCATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
 1572 TTGACGAACCACTAAATTCGGCATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631  
 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
 1632 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 1675

RESULT 29  
 US-09-481-355-23  
 ; Sequence 23, Application US/09481355  
 ; Patent No. 6524824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003F  
 ; CURRENT APPLICATION NUMBER: US/09/481,355  
 ; PRIOR FILING DATE: 2000-01-12  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR FILING DATE: 1997-09-26  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 23  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-481-355-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTCTCTGTTGAGAGTCTGAGTAGTGTGCGGAGCAAAATTTAGCTACA 60  
 DB 1152 CTGCTCCCTCTCTGTTGAGAGTCTGAGTAGTGTGCGGAGCAAAATTTAGCTACA 1211  
 QY 61 ACAAGGCAAGGCTTGACCGACAATTCATGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 120  
 DB 1212 ACAAGGCAAGGCTTGACCGACAATTCATGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 1271  
 QY 121 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 180  
 DB 1272 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 1331  
 QY 181 CGAAAGCGGGGCTTCGGTTGACGGCAATTCGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 240  
 DB 1332 CGCCAGCGGGGCTTCGGTTGACGGCAATTCGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
 DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 1451  
 QY 301 TAAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 360  
 DB 1452 TAAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 1511  
 QY 361 TGAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 420  
 DB 1512 TGAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 1571  
 QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479  
 DB 1572 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 1631  
 QY 480 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 DB 1632 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 30

US-09-481-355-28  
 ; Sequence 28, Application US/09481355  
 ; Patent No. 6524824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003F  
 ; CURRENT FILING DATE: 2000-01-12  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 28  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)

OTHER INFORMATION: a, c, t, g, other or unknown  
 NAME/KEY: modified\_base  
 LOCATION: (8499)  
 OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-481-355-28  
 Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTCTCTGTTGAGAGTCTGAGTAGTGTGCGGAGCAAAATTTAGCTACA 60  
 DB 1152 CTGCTCCCTCTCTGTTGAGAGTCTGAGTAGTGTGCGGAGCAAAATTTAGCTACA 1211  
 QY 61 ACAAGGCAAGGCTTGACCGACAATTCATGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 120  
 DB 1212 ACAAGGCAAGGCTTGACCGACAATTCATGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 1271  
 QY 121 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 180  
 DB 1272 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 1331  
 QY 181 CGAAAGCGGGGCTTCGGTTGACGGCAATTCGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 240  
 DB 1332 CGCCAGCGGGGCTTCGGTTGACGGCAATTCGATGAGATCTGCTTAGGCTTAGGCGTTTTCGG 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
 DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 1451  
 QY 301 TAAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 360  
 DB 1452 TAAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 1511  
 QY 361 TGAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 420  
 DB 1512 TGAAGTAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGCATGCCGATTGG 1571  
 QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479  
 DB 1572 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 1631  
 QY 480 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 DB 1632 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 31

US-09-481-282-22  
 ; Sequence 22, Application US/09481282  
 ; Patent No. 6541221  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003US  
 ; CURRENT FILING DATE: 2000-01-11  
 ; PRIOR APPLICATION NUMBER: 09/481,282  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 9737  
 ; TYPE: DNA

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RESULT 33
US-09-481-282-28
; Sequence 28, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223

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; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; TYPE: DNA
; LENGTH: 9737
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-28

Query Match          95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1211

QY 61 ACAAGCAGAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTTAAGCTACA 120
DB 1212 ACAAGCAGAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTTAAGCTACA 1271

QY 121 CTGCTCCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 1272 CTGCTCCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 1331

QY 181 CGAAAGCGGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 240
DB 1332 CGCCAGCGGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 1391

QY 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG 1451
DB 1392 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG 1451

QY 301 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
DB 1452 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1511

QY 361 TGGAGTAAAGTGTGATCGATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 420
DB 1512 TGGAGTAAAGTGTGATCGATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 1571

QY 421 TTGGAGAACCACTAAATTCGGCATTCGAGAT-ATTGTATTAGTGTGCTAGCTCGAT 479
DB 1572 TTGGAGAACCACTAAATTCGGCATTCGAGAT-ATTGTATTAGTGTGCTAGCTCGAT 1631

RESULT 34
US-09-455-659A-22
; Sequence 22, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERE, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A

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; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

Query Match          95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1211

QY 61 ACAAGCAGAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTTAAGCTACA 120
DB 1212 ACAAGCAGAGGCTTGACCGCAATTCGATGAGTGTGCGGAGCAAAATTTAAGCTACA 1271

QY 121 CTGCTCCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 1272 CTGCTCCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 1331

QY 181 CGAAAGCGGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 240
DB 1332 CGCCAGCGGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 1391

QY 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG 300
DB 1392 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG 1451

QY 301 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
DB 1452 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1511

QY 361 TGGAGTAAAGTGTGATCGATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 420
DB 1512 TGGAGTAAAGTGTGATCGATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA 1571

QY 421 TTGGAGAACCACTAAATTCGGCATTCGAGAT-ATTGTATTAGTGTGCTAGCTCGAT 479
DB 1572 TTGGAGAACCACTAAATTCGGCATTCGAGAT-ATTGTATTAGTGTGCTAGCTCGAT 1631

RESULT 35
US-09-455-659A-23
; Sequence 23, Application US/09455659A
; Patent No. 6602686

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GENERAL INFORMATION:  
 APPLICANT: HARRINGTON, JOHN J.  
 APPLICANT: SHERF, BRUCE  
 APPLICANT: RUNDLETT, STEPHEN  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 TITLE OF INVENTION: ENDOGENOUS GENES  
 FILE REFERENCE: 0221-0003A  
 CURRENT APPLICATION NUMBER: US/09/455,659A  
 CURRENT FILING DATE: 1999-12-07  
 PRIOR APPLICATION NUMBER: 09/276,820  
 PRIOR FILING DATE: 1999-03-26  
 PRIOR APPLICATION NUMBER: 09/263,814  
 PRIOR FILING DATE: 1999-03-08  
 PRIOR APPLICATION NUMBER: 09/253,022  
 PRIOR FILING DATE: 1999-02-19  
 PRIOR APPLICATION NUMBER: 09/159,643  
 PRIOR FILING DATE: 1998-09-24  
 PRIOR APPLICATION NUMBER: 08/941,223  
 PRIOR FILING DATE: 1997-09-26  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 23  
 LENGTH: 9737  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: modified\_base  
 LOCATION: (8347)  
 OTHER INFORMATION: a, c, t, g, other or unknown  
 FEATURE:  
 NAME/KEY: modified\_base  
 LOCATION: (8499)  
 OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-455-659A-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 1211  
 QY 61 ACAAGGCAAGGCTTACCGCAATTCATGAAGAAATCTGTTAGGGTTAGCGGTTTGG 120  
 Db 1212 ACAAGGCAAGGCTTACCGCAATTCATGAAGAAATCTGTTAGGGTTAGCGGTTTGG 1271  
 QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 1272 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1331  
 QY 181 CGAAAAGCGGGCTTTCGGTTGACGGGTTAGGAGTCCCTCAGAGATATAGTATTGCG 240  
 Db 1332 CGCCAGCGGGCTTTCGGTTGACGGGTTAGGAGTCCCTCAGAGATATAGTATTGCG 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACATCTCTGAGGTTAGGTTTGG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACATCTCTGAGGTTAGGTTTGG 1451  
 QY 301 TAACGATGATGTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 360  
 Db 1452 TAACGATGATGTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 1511  
 QY 361 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
 Db 1512 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 1571  
 QY 421 TTGAGCAACACCTAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 479  
 Db 1572 TTGAGCAACACCTAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCG 1631  
 QY 480 ACAATAAGCGCATTTGACCATTCACCATTTGCTGTCGCACTTC 523

Db 1632 ACAATAAGCGCATTTGACCATTCACCATTTGCTGTCGCACTTC 1675  
 RESULT 36  
 US-09-455-659A-28  
 Sequence 28, Application US/09455659A  
 Patent No. 6602686  
 GENERAL INFORMATION:  
 APPLICANT: HARRINGTON, JOHN J.  
 APPLICANT: SHERF, BRUCE  
 APPLICANT: RUNDLETT, STEPHEN  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 TITLE OF INVENTION: ENDOGENOUS GENES  
 FILE REFERENCE: 0221-0003A  
 CURRENT APPLICATION NUMBER: US/09/455,659A  
 CURRENT FILING DATE: 1999-12-07  
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 PRIOR FILING DATE: 1999-03-26  
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 PRIOR APPLICATION NUMBER: 09/253,022  
 PRIOR FILING DATE: 1999-02-19  
 PRIOR APPLICATION NUMBER: 09/159,643  
 PRIOR FILING DATE: 1998-09-24  
 PRIOR APPLICATION NUMBER: 08/941,223  
 PRIOR FILING DATE: 1997-09-26  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 28  
 LENGTH: 9737  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: modified\_base  
 LOCATION: (8347)  
 OTHER INFORMATION: a, c, t, g, other or unknown  
 FEATURE:  
 NAME/KEY: modified\_base  
 LOCATION: (8499)  
 OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-455-659A-28

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 1211  
 QY 61 ACAAGGCAAGGCTTACCGCAATTCATGAAGAAATCTGTTAGGGTTAGCGGTTTGG 120  
 Db 1212 ACAAGGCAAGGCTTACCGCAATTCATGAAGAAATCTGTTAGGGTTAGCGGTTTGG 1271  
 QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 1272 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1331  
 QY 181 CGAAAAGCGGGCTTTCGGTTGACGGGTTAGGAGTCCCTCAGAGATATAGTATTGCG 240  
 Db 1332 CGCCAGCGGGCTTTCGGTTGACGGGTTAGGAGTCCCTCAGAGATATAGTATTGCG 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACATCTCTGAGGTTAGGTTTGG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACATCTCTGAGGTTAGGTTTGG 1451  
 QY 301 TAACGATGATGTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 360  
 Db 1452 TAACGATGATGTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 1511  
 QY 361 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
 Db 1512 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 1571

QY 421 TTGACGACCACTAAATTCGGATTCAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 479  
 Db 1572 TTGACGACCACTAAATTCGGATTCAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 1631  
 QY 480 ACAATAAGCCCAATTCACCAATTCACCAATTCGTCGACCTC 523  
 Db 1632 ACAATAAGCCCAATTCACCAATTCACCAATTCGTCGACCTC 1675

RESULT 37  
 US-09-484-996-22  
 ; Sequence 22, Application US/09484996  
 ; Patent No. 6623958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003H  
 ; CURRENT APPLICATION NUMBER: US/09/484,996  
 ; PRIOR FILING DATE: 2000-01-18  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1998-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-484-996-22

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 1211  
 QY 61 ACAAGCAGGCTTGACCGCAATTCATGAGTAATCTGTTAGGGTAGGCGTTTTCG 120  
 Db 1212 ACAAGCAGGCTTGACCGCAATTCATGAGTAATCTGTTAGGGTAGGCGTTTTCG 1271  
 QY 121 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 1211  
 Db 1272 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 1211  
 QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTCAGAGTCCCTCAGGATATAGTATTCGC 240  
 Db 1332 CGCCAGCGGGCTTCGGTTGTACGGGTCAGAGTCCCTCAGGATATAGTATTCGC 240  
 QY 241 TTTTGCATAGGAGGGGAAATGACTCTTATGCAATCTCTTGTAGTCTTTGCAATCG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGACTCTTATGCAATCTCTTGTAGTCTTTGCAATCG 300  
 QY 301 TAAAGATGATTAGCAACATGCTTTACAGGAGGAGAAACCGTGCATTCGCGATTGG 360

Db 1452 TAACGATGAGTTAGCAACATGCCCTTAAGGAGAGAAAGCAACCGTGCATCCGATTGG 1511  
 QY 361 TGGAGTAAGGTCGTAACGATCGTCCCTTATTAGGAGGCAACAGCGGCTTGACATTGA 420  
 Db 1512 TGGAGTAAGGTCGTAACGATCGTCCCTTATTAGGAGGCAACAGCGGCTTGACATTGA 1571  
 QY 421 TTGACGACCACTAAATTCGGATTCAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 479  
 Db 1572 TTGACGACCACTAAATTCGGATTCAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 1631  
 QY 480 ACAATAAGCCCAATTCACCAATTCACCAATTCGTCGACCTC 523  
 Db 1632 ACAATAAGCCCAATTCACCAATTCACCAATTCGTCGACCTC 1675

RESULT 38  
 US-09-484-996-23  
 ; Sequence 23, Application US/09484996  
 ; Patent No. 6623958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003H  
 ; CURRENT APPLICATION NUMBER: US/09/484,996  
 ; PRIOR FILING DATE: 2000-01-18  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1998-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 23  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-484-996-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 1211  
 QY 61 ACAAGCAGGCTTGACCGCAATTCATGAGTAATCTGTTAGGGTAGGCGTTTTCG 120  
 Db 1212 ACAAGCAGGCTTGACCGCAATTCATGAGTAATCTGTTAGGGTAGGCGTTTTCG 1271  
 QY 121 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 1211  
 Db 1272 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTACA 1211  
 QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTCAGAGTCCCTCAGGATATAGTATTCGC 240  
 Db 1332 CGCCAGCGGGCTTCGGTTGTACGGGTCAGAGTCCCTCAGGATATAGTATTCGC 240  
 QY 241 TTTTGCATAGGAGGGGAAATGACTCTTATGCAATCTCTTGTAGTCTTTGCAATCG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGACTCTTATGCAATCTCTTGTAGTCTTTGCAATCG 300  
 QY 301 TAAAGATGATTAGCAACATGCTTTACAGGAGGAGAAACCGTGCATTCGCGATTGG 360

Db	1272	CTGCTTCGGGATGTACGGGCCAGATATACGGTATCTGAGGGGACTAGGTTGTGTTAGG	1331
Qy	181	CGAAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATATAGTATGTTCCG	240
Db	1332	CGCCACAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATATAGTATGTTCCG	1391
Qy	241	TTTTCGATAGGAGGGGGAAATGTAAGTCTTATGCAATPACTCTTGTAGTCTTGTCAAATGG	300
Db	1392	TTTTCGATAGGAGGGGGAAATGTAAGTCTTATGCAATPACTCTTGTAGTCTTGTCAAATGG	1451
Qy	301	TACGATGAGTTAGCAACATGCCTTACAGGAGAGAAAGCACCGTGCATGCCGATTTGG	360
Db	1452	TACCATGAGTTAGCAACATGCCTTACAGGAGAGAAAGCACCGTGCATGCCGATTTGG	1511
Qy	361	TGGAGTAAAGTGTTAGCATCGTGCCCTTATTAGCAAGGCAACAGACGGGCTCGACATGA	420
Db	1512	TGGAGTAAAGTGTTAGCATCGTGCCCTTATTAGCAAGGCAACAGACGGGCTCGACATGA	1571
Qy	421	TTTGGACAAACCACTAAATTCGCATTTGCAGATGTCAGAGAT-ATTGTATTTAAAGTCCTAGCTCGAT	479
Db	1572	TTTGGACAAACCACTAAATTCGCATTTGCAGAGATTTGTATTTTAAAGTCCTAGCTCGAT	1631
Qy	480	ACAATAAACGCCATTGTGACATTTCAACCAATTTGGTGTGCACCTC	523
Db	1632	ACAATAAACGCCATTGTGACATTTCAACCAATTTGGTGTGCACCTC	1675

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1572 TTGGACGAAACCACTGAATTCCGCGATTTCGACAGATAAATTGTTATTTAAGTGCCTAGCTCGAT 1675
QY      480 ACAATAAAAGCCATTGGACCAATTACCAACATTTGGTGTGCACCTC 523
      |||||
Db      1632 ACAATAAAAGCCATTGGACCAATTACCCACATTTGGTGTGCACCTC 1675

RESULT 40
US-09-479-123-22
; Sequence 22, Application US/09479123
; Patent NO. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RONDETTI, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatencIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-479-123-22

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FEATURE:
NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
S-09-479-123-22

Query Match      95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-163;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Y      1  CTGCTCCCTGCTTGTTGAGTGCCTGAGTGTAGTCGCGAGCAAAATTTAGCTACA 60
      1152  CTGCTCCCTGCTTGTTGAGTGCCTGAGTGTAGTCGCGAGCAAAATTTAGCTACA 1211

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QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAGAAATCTCTTAGGTTAGGCTTTTGGG 120  
 DB 1212 ACAAGCAAGGCTTGACCGCAATTCGATGAGAAATCTCTTAGGTTAGGCTTTTGGG 1271  
 QY 121 CTGCTTCGCGATGTACCGGCGAGATATTCGCTATCTAGGCGGACTAGGCGTGTCTTTAGG 180  
 DB 1272 CTGCTTCGCGATGTACCGGCGAGATATTCGCTATCTAGGCGGACTAGGCGTGTCTTTAGG 1331  
 QY 181 CGAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTCTTCGC 240  
 DB 1332 CGCCAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTCTTCGC 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451  
 QY 301 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTTGG 360  
 DB 1452 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTTGG 1511  
 QY 361 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACAGACGGGCTCTGCATGGA 420  
 DB 1512 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACAGACGGGCTCTGCATGGA 1571  
 QY 421 TTGACGACACCTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 DB 1572 TTGACGACACCTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631  
 QY 480 ACAATAACGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
 DB 1632 ACAATAACGCCATTGACCATTCACCATTTGGTGTGCACCTC 1675

RESULT 41  
 US-09-479-123-23  
 ; Sequence 23, Application US/09479123  
 ; Patent No. 6670185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003B  
 ; CURRENT APPLICATION NUMBER: US/09/479,123  
 ; CURRENT FILING DATE: 2000-01-07  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 23  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; US-09-479-123-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTCTTGTCTTGGAGTGTCTAGTGTAGTGGCGGAGCAAAATTTTAACTACA 60  
 DB 1152 CTGCTCCCTCTTGTCTTGGAGTGTCTAGTGTAGTGGCGGAGCAAAATTTTAACTACA 1211  
 QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAGAAATCTCTTAGGTTAGGCTTTTGGG 120  
 DB 1212 ACAAGCAAGGCTTGACCGCAATTCGATGAGAAATCTCTTAGGTTAGGCTTTTGGG 1271  
 QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTAGGCGGACTAGGCGTGTCTTTAGG 180  
 DB 1272 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTAGGCGGACTAGGCGTGTCTTTAGG 1331  
 QY 181 CGAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTCTTCGC 240  
 DB 1332 CGCCAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTCTTCGC 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451  
 QY 301 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTTGG 360  
 DB 1452 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTTGG 1511  
 QY 361 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACAGACGGGCTCTGCATGGA 420  
 DB 1512 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACAGACGGGCTCTGCATGGA 1571  
 QY 421 TTGACGACACCTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 DB 1572 TTGACGACACCTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631  
 QY 480 ACAATAACGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
 DB 1632 ACAATAACGCCATTGACCATTCACCATTTGGTGTGCACCTC 1675

RESULT 42  
 US-09-479-123-28  
 ; Sequence 28, Application US/09479123  
 ; Patent No. 6670185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003B  
 ; CURRENT APPLICATION NUMBER: US/09/479,123  
 ; CURRENT FILING DATE: 2000-01-07  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 28  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; US-09-479-123-28



US-09-479-123-28

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Query Match          95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAGAAATCTGCTAGGGTTAGCGTTTGGG 120
DB 1212 ACAAGGCAAGGCTTGACCGACAAATTCATGAGAAATCTGCTAGGGTTAGCGTTTGGG 1271
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 180
DB 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 1331
QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGTTAGAGGTCCCTCAGGATATAGTATTTGGC 240
DB 1332 CGCCAGCGGGGCTTCGGTTGTACGGGTTAGAGGTCCCTCAGGATATAGTATTTGGC 1391
QY 241 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGCACATGG 300
DB 1392 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGCACATGG 1451
QY 301 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
DB 1452 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1511
QY 361 TGGAGTAAAGTGTGATGATCTGTCCTTATGAGAGGCAACAGACGGGTCTGACATGGA 420
DB 1512 TGGAGTAAAGTGTGATGATCTGTCCTTATGAGAGGCAACAGACGGGTCTGACATGGA 1571
QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGATATTCGATATTTAAGTGTGCTAGCTCGAT 479
DB 1572 TTGACGAAACCACTAAATTCGCAATTCGAGATATTCGATATTTAAGTGTGCTAGCTCGAT 1631
QY 480 ACAATAAAGCCATTGACCAATTCACCAATTCACCAATTCGATGTCGACCTC 523
DB 1632 ACAATAAAGCCATTGACCAATTCACCAATTCACCAATTCGATGTCGACCTC 1675

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RESULT 43

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US-09-479-122-24
; Sequence 24, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-24

Query Match          95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1286 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAGAAATCTGCTAGGGTTAGCGTTTGGG 120
DB 1346 ACAAGGCAAGGCTTGACCGACAAATTCATGAGAAATCTGCTAGGGTTAGCGTTTGGG 1405
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 180
DB 1406 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 1465
QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGTTAGAGGTCCCTCAGGATATAGTATTTGGC 240
DB 1466 CGCCAGCGGGGCTTCGGTTGTACGGGTTAGAGGTCCCTCAGGATATAGTATTTGGC 1525
QY 241 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGCACATGG 300
DB 1526 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGCACATGG 1585
QY 301 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
DB 1586 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1645
QY 361 TGGAGTAAAGTGTGATGATCTGTCCTTATGAGAGGCAACAGACGGGTCTGACATGGA 420
DB 1646 TGGAGTAAAGTGTGATGATCTGTCCTTATGAGAGGCAACAGACGGGTCTGACATGGA 1705
QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGATATTCGATATTTAAGTGTGCTAGCTCGAT 479
DB 1706 TTGACGAAACCACTAAATTCGCAATTCGAGATATTCGATATTTAAGTGTGCTAGCTCGAT 1765
QY 480 ACAATAAAGCCATTGACCAATTCACCAATTCACCAATTCGATGTCGACCTC 523
DB 1766 ACAATAAAGCCATTGACCAATTCACCAATTCACCAATTCGATGTCGACCTC 1809

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RESULT 44

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US-09-484-997-24
; Sequence 24, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-24

Query Match          95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7,1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 1286 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAACTCTGTAGGTTAGCGCTTTTGG 120
Db 1346 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAACTCTGTAGGTTAGCGCTTTTGG 1405
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db 1406 CTGCTTCGCGATGTACGGGCCAGATATTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1465
QY 181 CGAAAGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGAGTAATGATGTTTGG 240
Db 1466 CGCCAGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGAGTAATGATGTTTGG 1525
QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300
Db 1526 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1585
QY 301 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGG 360
Db 1586 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGG 1645
QY 361 TGGAGTAGGTTGAGTACGATCGCTTATTAGGAGGCAACAGACGGTCTGACATGA 420
Db 1646 TGGAGTAGGTTGAGTACGATCGCTTATTAGGAGGCAACAGACGGTCTGACATGA 1705
QY 421 TTGGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAGTGGCTAGCTCGAT 479
Db 1706 TTGGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAGTGGCTAGCTCGAT 1765
QY 480 ACAATAAGCGCATTTGACCAATTCACCAATTCGATGTTGTCACCTC 523
Db 1766 ACAATAAGCGCATTTGACCAATTCACCAATTCGATGTTGTCACCTC 1809

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RESULT 45
US-09-481-355-24
; Sequence 24, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: SHERE, BRUCE
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223

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; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-24

Query Match          95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7,1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 1286 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAACTCTGTAGGTTAGCGCTTTTGG 120
Db 1346 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAACTCTGTAGGTTAGCGCTTTTGG 1405
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db 1406 CTGCTTCGCGATGTACGGGCCAGATATTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1465
QY 181 CGAAAGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGAGTAATGATGTTTGG 240
Db 1466 CGCCAGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGAGTAATGATGTTTGG 1525
QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300
Db 1526 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1585
QY 301 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGG 360
Db 1586 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGG 1645
QY 361 TGGAGTAGGTTGAGTACGATCGCTTATTAGGAGGCAACAGACGGTCTGACATGA 420
Db 1646 TGGAGTAGGTTGAGTACGATCGCTTATTAGGAGGCAACAGACGGTCTGACATGA 1705
QY 421 TTGGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAGTGGCTAGCTCGAT 479
Db 1706 TTGGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAGTGGCTAGCTCGAT 1765
QY 480 ACAATAAGCGCATTTGACCAATTCACCAATTCGATGTTGTCACCTC 523
Db 1766 ACAATAAGCGCATTTGACCAATTCACCAATTCGATGTTGTCACCTC 1809

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RESULT 46
US-09-481-282-24
; Sequence 24, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERE, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282

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## RESULT 48

US-09-484-996-24  
; Sequence 24, Application US/09484996  
; Patent No. 6623958  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERP, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003H  
; CURRENT APPLICATION NUMBER: US/09/484,996  
; CURRENT FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1998-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 9871  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8481)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; NAME/KEY: modified\_base  
; LOCATION: (8633)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-484-996-24

Query Match 95.8%; Score 500.8; DB 4; Length 9871;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTTGGAGTCTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60  
DB 1286 CTGCTCCCTGCTTGTGTTGGAGTCTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 1345  
QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGTTAGCGTTTGGC 120  
DB 1346 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGTTAGCGTTTGGC 1405  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGTTGTTAGG 180  
DB 1406 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGTTGTTAGG 1465  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTCCG 240  
DB 1466 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTCCG 1525  
QY 241 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTGCAACATGG 300  
DB 1526 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTGCAACATGG 1585  
QY 301 TAACGATGATGACCAATCGCTTACAGGAGAGAAAGCAACCGTCATGCGGATTGG 360  
DB 1586 TAACGATGATGACCAATCGCTTACAGGAGAGAAAGCAACCGTCATGCGGATTGG 1645  
QY 361 TGGAGTAAAGTGTGACGTCGCTTATTAGAGGAGCAACAGACGGTCTGACATGA 420  
DB 1646 TGGAGTAAAGTGTGACGTCGCTTATTAGAGGAGCAACAGACGGTCTGACATGA 1705  
QY 421 TTGAGCAACCACTAAATTCGCATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
DB 1706 TTGAGCAACCACTAAATTCGCATTCAGAGATATTGTATTAAAGTGCCTAGCTCGAT 1765

QY 480 ACAATAAAGCCATTGTGACATTACCAATTTGGTGTGACCTC 523  
DB 1766 ACAATAAAGCCATTGTGACATTACCAATTTGGTGTGACCTC 1809  
RESULT 49  
US-09-479-123-24  
; Sequence 24, Application US/09479123  
; Patent No. 6670185  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERP, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003B  
; CURRENT APPLICATION NUMBER: US/09/479,123  
; CURRENT FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 9871  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8481)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; NAME/KEY: modified\_base  
; LOCATION: (8633)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-479-123-24

Query Match 95.8%; Score 500.8; DB 4; Length 9871;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTTGGAGTCTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60  
DB 1286 CTGCTCCCTGCTTGTGTTGGAGTCTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 1345  
QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGTTAGCGTTTGGC 120  
DB 1346 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGTTAGCGTTTGGC 1405  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGTTGTTAGG 180  
DB 1406 CTGCTTCGGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGTTGTTAGG 1465  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTCCG 240  
DB 1466 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTCCG 1525  
QY 241 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTGCAACATGG 300  
DB 1526 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTGCAACATGG 1585  
QY 301 TAACGATGATGACCAATCGCTTACAGGAGAGAAAGCAACCGTCATGCGGATTGG 360  
DB 1586 TAACGATGATGACCAATCGCTTACAGGAGAGAAAGCAACCGTCATGCGGATTGG 1645  
QY 361 TGGAGTAAAGTGTGACGTCGCTTATTAGAGGAGCAACAGACGGTCTGACATGA 420

Query Match	95.8%;	Score 500.8;	DE 4;	Length 10060;
Best Local Similarity	98.5%;	Pred. No. 7,2e-169;		
Matches 516;	Conservative 0;	Mismatches 7;	Indels 1;	Gaps 1;
QY	1	CTGCTCCCTCGCTGTGCTCTGGAGGTGCGCTAGGTAGTGGCGGAGCAAAATTTAACTACA	60	
Db	1475	CTGCTCCCTCGCTGTGCTCTGGAGGTGCGCTAGGTAGTGGCGGAGCAAAATTTAACTACA	1534	
QY	61	ACAAGCGAAGGCTTGACCGCAATTCGATGAAGAACTCGCTTAGGGTTAGGGGTTTTGCG	120	
Db	1535	ACAAGCGAAGGCTTGACCGCAATTCGATGAAGAACTCGCTTAGGGTTAGGGGTTTTGCG	1594	
QY	121	CTGCTTCGCGAGTACGGGCCAGATANTCGCGTATCTGAGGGGACCTAGGCTGTGTTTAGG	180	
Db	1595	CTGCTTCGCGATGTCAGGGGCCAGATATACGCGTATCTGAGGGGACCTAGGCTGTGTTTAGG	1654	
QY	181	CGAAAACGGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCGCTCAGGATATAGTAGTTTCGC	240	
Db	1655	CGCCACGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCGCTCAGGATATAGTAGTTTCGC	1714	
QY	241	TTTTTCATAGGAGGGGAAATGTAGCTTTATGCAATCTCTTGTAGCTCTTCGACATGCG	300	
Db	1715	TTTTTCATAGGAGGGGAAATGTAGCTTTATGCAATCTCTTGTAGCTCTTCGACATGCG	1774	

	Query Match	95.8%	Score 500.8	DB 4	Length 10060
	Best Local Similarity	98.5%	Pred. No. 7.2e-169		
	Matches 516	Conservative 0	Mismatches 7	Indels 1	Gaps 1
QY	1	CTGCTCCCTCTGTGTGTCTTGAGGTGCGTGTAGTAGTCGCGAGCAAAAATTAAAGCTACA	60		
Db	1475	CTGCTCCCTCTGTGTGTCTTGAGGTGCGTGTAGTAGTCGCGAGCAAAAATTAAAGCTACA	1534		
QY	61	ACAGGCAAGCGTTGACCGACAATTCGATGAAGAATCTGCTTAGGTTTAGCGGTTTTTGGC	120		
Db	1535	ACAGGCAAGCGTTGACCGACAATTCGATGAAGAATCTGCTTAGGTTTAGCGGTTTTTGGC	1594		
QY	121	CTGCTTGCAGATGTACGGGCGCAGATTCGCGGTATCTGAGGGGACTAGGGTGCTTTAGG	180		
Db	1595	CTGCTTGCAGATGTACGGGCGCAGATATACGGGTATCTGAGGGGACTAGGGTGCTTTAGG	1654		
QY	181	CGAAAAAGCGGGGCTTCGGTTGTACGGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC	240		

Db 1655 CGCCACGCGGGCTTCGGTTGTATGACGGGTTAGGAGTCCCTCAGGATATAGTAGTTGCG 1714

Qy 241 TTTTGGCTAGGAGGGGGAATAGTCTTATGCAATACCTCTGTAGTCTTGGCAATGG 300

Db 1715 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATACCTCTGTAGTCTTGGCAATGG 1774

Qy 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360

Db 1775 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1834

Qy 361 TGGAGTAAGTGGTACCAATCGTCTTATAGGAGGCAACAGCGGTCTGACATGA 420

Db 1835 TGGAGTAAGTGGTACCAATCGTCTTATAGGAGGCAACAGCGGTCTGACATGA 1894

Qy 421 TTGACGAACCACTAAATTCGGCAATGCGAGAT - ATTGTATTTAAGTGGTGCACCTC 479

Db 1895 TTGACGAACCACTAAATTCGGCAATGCGAGAT - ATTGTATTTAAGTGGTGCACCTC 1954

Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGGTGCACCTC 523

Db 1955 ACAATAAGCCATTGACCAATTCACCAATTTGGTGGTGCACCTC 1998

RESULT 52

US-09-481-355-25

; Sequence 25, Application US/09481355

; Patent No. 6524824

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERP, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; TITLE OF INVENTION: ENDOGENOUS GENES

; FILE REFERENCE: 0221-0003F

; CURRENT APPLICATION NUMBER: US/09/481,355

; CURRENT FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 10060

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8670)

; OTHER INFORMATION: a, c, t, g, other or unknown

; NAME/KEY: modified\_base

; LOCATION: (8822)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-481-355-25

Query Match 95.8%; Score 500.8; DB 4; Length 10060;

Best local Similarity 98.5%; Pred. No. 7.2e-169;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60

Db 1475 CTGCTCCCTCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1534

Qy 61 ACAAGGCAAGGCTTACCGCAATTCGCAATTCGCAATTCGCTTAGGCTTAGGCTTTGCG 120

Db 1535 ACAAGGCAAGGCTTACCGCAATTCGCAATTCGCAATTCGCTTAGGCTTAGGCTTTGCG 1594

Qy 121 CTGCTTCGATGATGAGGCGCAGATATTCGCTATCTGAGGGACTAGGCTGTGTTAGG 180

Db 1595 CTGCTTCGATGATGAGGCGCAGATATTCGCTATCTGAGGGACTAGGCTGTGTTAGG 1654

Qy 181 CGAAAAAGCGGGGCTTCGGTTCTAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTGCG 240

Db 1655 CGCCACGCGGGGCTTCGGTTCTAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTGCG 1714

Qy 241 TTTTGCATAGGAGGGGGAATGATGATCTTATGCAATCTCTTGTAGTCTTGCACATGG 300

Db 1715 TTTTGCATAGGAGGGGGAATGATGATCTTATGCAATCTCTTGTAGTCTTGCACATGG 1774

Qy 301 TAAAGTATGATGATGACCAATCCCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360

Db 1775 TAAAGTATGATGACCAATCCCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1834

Qy 361 TGGAGTAAGTGGTACCAATCGTCTTATAGGAGGCAACAGCGGTCTGACATGA 420

Db 1835 TGGAGTAAGTGGTACCAATCGTCTTATAGGAGGCAACAGCGGTCTGACATGA 1894

Qy 421 TTGACGAACCACTAAATTCGGCAATGCGAGAT - ATTGTATTTAAGTGGTGCACCTC 479

Db 1895 TTGACGAACCACTAAATTCGGCAATGCGAGAT - ATTGTATTTAAGTGGTGCACCTC 1954

Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGGTGCACCTC 523

Db 1955 ACAATAAGCCATTGACCAATTCACCAATTTGGTGGTGCACCTC 1998

RESULT 53

US-09-481-282-25

; Sequence 25, Application US/09481282

; Patent No. 6541221

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERP, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; TITLE OF INVENTION: ENDOGENOUS GENES

; FILE REFERENCE: 0221-0003US

; CURRENT APPLICATION NUMBER: US/09/481,282

; CURRENT FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 10060

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8670)

; OTHER INFORMATION: a, c, t, g, other or unknown

; NAME/KEY: modified\_base

; LOCATION: (8822)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-481-282-25

Query Match 95.8%; Score 500.8; DB 4; Length 10060;

Best local Similarity 98.5%; Pred. No. 7.2e-169;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60

Db 1475 CTGCTCCCTCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1534

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QY 61 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTTCGG 120
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|
Db 1535 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTTCGG 1594
|
|
|
QY 121 CTGCTTCGGATGTACGGGCGAGATATTCGGCTATCTGAGGGAATAGGTTAGG 180
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|
Db 1595 CTGCTTCGGATGTACGGGCGAGATATTCGGCTATCTGAGGGAATAGGTTAGG 1654
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|
|
QY 181 CGAAAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTTCGC 240
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Db 1655 CGCCAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTTCGC 1714
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|
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGAGTCTTGCACATGG 300
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Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGAGTCTTGCACATGG 1774
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|
QY 301 TAACGATGATGTAGCAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360
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|
Db 1775 TAACGATGATGTAGCAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1834
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QY 361 TGGAGTAAGGTGTAGTACGTCGTGCTTATAGGAGGCAACAGACGGGCTGACATGGA 420
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|
Db 1835 TGGAGTAAGGTGTAGTACGTCGTGCTTATAGGAGGCAACAGACGGGCTGACATGGA 1894
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|
|
QY 421 TTGACGCAACCACTAAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 479
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|
|
Db 1895 TTGACGCAACCACTAAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1954
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QY 480 ACAATAAGCGCATTTGACCATTCACCATTCAGCATTTGGTGACCTC 523
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Db 1955 ACAATAAGCGCATTTGACCATTCACCATTCAGCATTTGGTGACCTC 1998
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RESULT 54

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US-09-455-659A-25
; Sequence 25, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: modified_base
; LOCATION: (8670)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8670)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-455-659A-25

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Query Match 95.8%; Score 500.8; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 7.2e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 1 CTGCTTCCTCTGTTGTGTTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTTAAGCTTACA 60
|
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Db 1475 CTGCTTCCTCTGTTGTGTTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTTAAGCTTACA 1534
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QY 61 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTTCGG 120
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Db 1535 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTTCGG 1594
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|
|
QY 121 CTGCTTCGGATGTACGGGCGAGATATTCGGCTATCTGAGGGAATAGGTTAGG 180
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|
Db 1595 CTGCTTCGGATGTACGGGCGAGATATTCGGCTATCTGAGGGAATAGGTTAGG 1654
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QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGAGTCTTGCACATGG 300
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Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGAGTCTTGCACATGG 1774
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|
QY 301 TAACGATGATGTAGCAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360
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|
Db 1775 TAACGATGATGTAGCAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1834
|
|
|
QY 361 TGGAGTAAGGTGTAGTACGTCGTGCTTATAGGAGGCAACAGACGGGCTGACATGGA 420
|
|
|
Db 1835 TGGAGTAAGGTGTAGTACGTCGTGCTTATAGGAGGCAACAGACGGGCTGACATGGA 1894
|
|
|
QY 421 TTGACGCAACCACTAAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 479
|
|
|
Db 1895 TTGACGCAACCACTAAATTCGGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1954
|
|
|
QY 480 ACAATAAGCGCATTTGACCATTCACCATTCAGCATTTGGTGACCTC 523
|
|
|
Db 1955 ACAATAAGCGCATTTGACCATTCACCATTCAGCATTTGGTGACCTC 1998
|
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|

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RESULT 55

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US-09-484-996-25
; Sequence 25, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: modified_base
; LOCATION: (8670)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-996-25

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; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-25

Query Match          95.8%; Score 500.8; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 7.2e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
Db 1475 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 1534
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGGG 120
Db 1535 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGGG 1594
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 180
Db 1595 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 1654
QY 181 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 240
Db 1655 CGCCCAGGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 1714
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1774
QY 301 TAACGATGATGTAGCAATGCGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
Db 1775 TAACGATGATGTAGCAATGCGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1834
QY 361 TGGAGTAGAGTGTGAGTCGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420
Db 1835 TGGAGTAGAGTGTGAGTCGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1894
QY 421 TTGGACGAACCACTAAATTCGCGATTTGCGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 479
Db 1955 ACAATAAGCGCAATTCACCAATTCACCAATTCGCGATTTGCGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 1954

RESULT 56
US-09-479-123-25
; Sequence 25, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 09/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-25

Query Match          95.8%; Score 500.8; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 7.2e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
Db 1475 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 1534
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGGG 120
Db 1535 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTTGGG 1594
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 180
Db 1595 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTTGG 1654
QY 181 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 240
Db 1655 CGCCCAGGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 1714
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1774
QY 301 TAACGATGATGTAGCAATGCGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360
Db 1775 TAACGATGATGTAGCAATGCGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1834
QY 361 TGGAGTAGAGTGTGAGTCGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420
Db 1835 TGGAGTAGAGTGTGAGTCGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1894
QY 421 TTGGACGAACCACTAAATTCGCGATTTGCGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 479
Db 1895 TTGGACGAACCACTAAATTCGCGATTTGCGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 1954

RESULT 57
US-09-167-322-13
; Sequence 13, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/167,322
/ FILING DATE: 07-Oct-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US97/00582
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monago, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 7933-33 PC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 565 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-167-322-13

Query Match          90.2%; Score 472; DB 4; Length 565;
Best Local Similarity 98.0%; Pred. No. 3.1e-159;
Matches 490; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

QY 28 GCTGAGTATGTCGGAGCAAAATTTAAGCTACAAAGCAAGGCTTGACGCAATATGC 87
Db 1 GCTGAGTATGTCGGAGCAAAATTTAAGCTACAAAGCAAGGCTTGACGCAATATGC 60

QY 88 ATGAGAAATCTGTTAGGCTTTAGGCTTTGCGCTGCTTCGCGATGTACGGGCGAGAT 147
Db 61 ATGAGAAATCTGTTAGGCTTTAGGCTTTGCGCTGCTTCGCGATGTACGGGCGAGAT 120

QY 148 TCGCGTATCTAGGGGACTAGGCTGTGTTAGGGGAAAGCGGGCTTCGGTTGACGCG 207
Db 121 AGCGGTATCTAGGGGACTAGGCTGTGTTAGGGGAAAGCGGGCTTCGGTTGACGCG 180

QY 208 GTTAGAGTCCCTCAGGATATAGTATGCTTTGCTATGAGGAGGGGAAATGTAGT 267
Db 181 GTTAGAGTCCCTCAGGATATAGTATGCTTTGCTATGAGGAGGGGAAATGTAGT 240

QY 268 CTTATGCAATACTTGTAGTCTTGCACATG-----GTAAGATGAGTTAGCAACATGC 322
Db 241 CTTATGCAATACTTGTAGTCTTGCACATGTTTATGTAACATGAGTTAGCAACATGC 300

QY 323 CTTACAGAGAGAGAAAGCCGTCATGCCGATTGTTGGAAGTGAAGTGAATCG 382
Db 301 CTTACAGAGAGAGAAAGCCGTCATGCCGATTGTTGGAAGTGAAGTGAATCG 360

QY 383 TGCCCTATTAGGAGGCAACAGACGGGCTTGACATGATTGACGAACCACTAAATTCGG 442
Db 361 TGCCCTATTAGGAGGCAACAGACGGGCTTGACATGATTGACGAACCACTAAATTCGG 420

QY 443 CATTTGAGAGATATGTTATTAAGTCTGCTAGCTGATACAATAACCCCATTTGACCAAT 502
Db 421 CATTTGAGAGATATGTTATTAAGTCTGCTAGCTGATACAATAACCCCATTTGACCAAT 480

QY 503 CACCACATTTGTTGCACT 522
Db 481 CACCACATTTGTTGCACT 500

RESULT 58
US-09-470-881-1
; Sequence 1, Application US/09470861
; Patent No. 6685938
; GENERAL INFORMATION:
; APPLICANT: CHERESH, David A.
; APPLICANT: ELICEIRI, Brian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
/ TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
/ TITLE OF INVENTION: YES TYROSINE KINASES
/ FILE REFERENCE: TSSI 551.2
/ CURRENT APPLICATION NUMBER: US/09/470,881
/ CURRENT FILING DATE: 1999-12-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11780
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/087,220
/ PRIOR FILING DATE: 1998-05-29
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 11627
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: RCASBP(A) based
/ OTHER INFORMATION: on avian sarcoma virus
/ NAME/KEY: misc feature
/ LOCATION: (7649)..(11258)
/ OTHER INFORMATION: pBR322 sequences
/ NAME/KEY: LTR
/ LOCATION: (7166)..(7494)
/ OTHER INFORMATION: upstream
/ NAME/KEY: LTR
/ LOCATION: (1)..(101)
/ OTHER INFORMATION: upstream (numbering begins at the upstream R)
/ NAME/KEY: misc feature
/ LOCATION: (11394)..(11623)
/ OTHER INFORMATION: U3
/ NAME/KEY: misc feature
/ LOCATION: (1)..(21)
/ OTHER INFORMATION: R
/ NAME/KEY: misc feature
/ LOCATION: (22)..(101)
/ OTHER INFORMATION: U5
/ NAME/KEY: misc feature
/ LOCATION: (102)..(119)
/ NAME/KEY: LTR
/ LOCATION: (7166)..(7494)
/ OTHER INFORMATION: downstream
/ NAME/KEY: misc feature
/ LOCATION: (7166)..(7393)
/ OTHER INFORMATION: U3
/ NAME/KEY: misc feature
/ LOCATION: (7394)..(7414)
/ OTHER INFORMATION: R
/ NAME/KEY: misc feature
/ LOCATION: (7415)..(7494)
/ OTHER INFORMATION: U5
/ NAME/KEY: misc feature
/ LOCATION: (7154)..(7165)
/ OTHER INFORMATION: PPT
/ NAME/KEY: misc feature
/ LOCATION: (388)..(391)
/ OTHER INFORMATION: splice donor (AGGT)
/ NAME/KEY: misc feature
/ LOCATION: (5074)..(5077)
/ OTHER INFORMATION: env splice acceptor (AGGC)
/ NAME/KEY: misc feature
/ LOCATION: (6982)..(6985)
/ OTHER INFORMATION: C1a1 splice acceptor (AGGA)
/ NAME/KEY: gene
/ LOCATION: (372)..(902)
/ OTHER INFORMATION: gag p19
/ NAME/KEY: gene
/ LOCATION: (909)..(1094)
/ OTHER INFORMATION: gag p10
/ NAME/KEY: gene
/ LOCATION: (1095)..(1814)
/ OTHER INFORMATION: gag p27
/ NAME/KEY: gene
/ LOCATION: (1843)..(2108)

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; OTHER INFORMATION: gag p12
; NAME/KEY: gene
; LOCATION: (2109)..(2480)
; OTHER INFORMATION: gag p15
; NAME/KEY: misc_signal
; LOCATION: (2481)..(2483)
; OTHER INFORMATION: gag stop
; NAME/KEY: gene
; LOCATION: (2501)..(4216)
; OTHER INFORMATION: pol RT
; NAME/KEY: gene
; LOCATION: (4217)..(5185)
; OTHER INFORMATION: pol IN
; NAME/KEY: misc_signal
; LOCATION: (5186)..(5188)
; OTHER INFORMATION: pol stop
; NAME/KEY: gene
; LOCATION: (5244)..(6263)
; OTHER INFORMATION: env gp85
; NAME/KEY: gene
; LOCATION: (6264)..(6878)
; OTHER INFORMATION: env gp37
; NAME/KEY: misc_signal
; LOCATION: (6879)..(6981)
; OTHER INFORMATION: env stop
; NAME/KEY: misc_feature
; LOCATION: (7027)
; OTHER INFORMATION: ClaI site/ the ClaI site in gag is methylated in
; OTHER INFORMATION: Dam+ strains and does not cut
US-09-470-881-1

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Query Match      74.6%; Score 390.2; DB 4; Length 11627;
Best Local Similarity 99.2%; Pred. No. 3.9e-129;
Matches 392; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 128 GCGATCTAGCGGCGAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGCGGAAG 187
Db 7034 GCGATGTCGCGGCGAGATATACCGCTATCTGAGGGGACTAGGCTGTGTTAGCGGAAG 7093

QY 188 CGGGGCTCGGTTGACGCGGTAGGAGTCCCTCAGGATATAGTAGTTCGCTTTTGA 247
Db 7094 CGGGGCTCGGTTGACGCGGTAGGAGTCCCTCAGGATATAGTAGTTCGCTTTTGA 7153

QY 248 TAGGGAGGGGAAATAGTCTTATGCAATATCTCTTAGTCTTGCAACATGTTAGCAT 307
Db 7154 TAGGGAGGGGAAATAGTCTTATGCAATATCTCTTAGTCTTGCAACATGTTAGCAT 7213

QY 308 GAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTCATGCCGATTGTTGAAGT 367
Db 7214 GAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTCATGCCGATTGTTGAAGT 7273

QY 368 AAGTGTTACGATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGAATTGACG 427
Db 7274 AAGTGTTACGATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGAATTGACG 7333

QY 428 AACCATTAATTCGCGATTCGAGAGATATGTTATTAAGTGCCTAGCTCGATCAATATA 487
Db 7334 AACCATTAATTCGCGATTCGAGAGATATGTTATTAAGTGCCTAGCTCGATCAATATA 7393

QY 488 CGCCATTTGACCATTCACCATTTGGTGTGCACCT 522
Db 7394 CGCCATTTGACCATTCACCATTTGGTGTGCACCT 7428

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RESULT 59
US-08-972-218-2
; Sequence 2, Application US/08972218
; Patent No. 6197502
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James B.

```

```

; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-972-218-2

Query Match      39.2%; Score 205.2; DB 3; Length 9521;
Best Local Similarity 98.6%; Pred. No. 8.5e-63;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 AYTAGTCTTATGCAATATCTCTTGTAGTCTTGCAACATGTTAGTGTAGCAACAT 320
Db 664 ATCCAGTCTTATGCAATATCTCTTGTAGTCTTGCAACATGTTAGTGTAGCAACAT 723

QY 321 GCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGTTGGAAGTAAAGTGTAGCAT 380
Db 724 GCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGTTGGAAGTAAAGTGTAGCAT 783

QY 381 CGTCCCTTATTAGGAAGCAACAGACGGGTCTGTGACATGTTGACGAACCACTAAATTC 440
Db 784 CGTCCCTTATTAGGAAGCAACAGACGGGTCTGTGACATGTTGACGAACCACTAAATTC 843

QY 441 CGCATTCAGAGATATTCATTAAAGTGC 470
Db 844 CGCATTCAGAGATATTCATTAAAGTGC 873

RESULT 60
US-09-193-707-2
; Sequence 2, Application US/09193707
; Patent No. 6524792
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James B.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,
; TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WITH
; TITLE OF INVENTION: A PREDETERMINED PROPERTY
; FILE REFERENCE: 8358-0005-999

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; CURRENT APPLICATION NUMBER: US/09/193,707  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 9521  
; TYPE: DNA  
; ORGANISM: Alphavirus, Sindbis Virus  
US-09-193-707-2

Query Match 39.2%; Score 205.2; DB 4; Length 9521;  
Best Local Similarity 98.6%; Pred. No. 8.5e-63;  
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTTAAACATGAGTTAGCAACAT 320  
Db |||  
664 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTTAAACATGAGTTAGCAACAT 723  
QY 321 GCCTTACAG 380  
Db |||  
724 GCCTTACAG 783  
QY 381 CGTGCCTTATTAGGAGGAG 440  
Db |||  
784 CGTGCCTTATTAGGAGGAG 843  
QY 441 CGCATTCGAGAGATATTGTTATTTAAAGTGCC 470  
Db |||  
844 CGCATTCGAGAGATATTGTTATTTAAAGTGCC 873

RESULT 61  
US-09-733-042-1  
; Sequence 1, Application US/09733042  
; Patent No. 6576443  
; GENERAL INFORMATION:  
; APPLICANT: Hennecke, Frank  
; APPLICANT: Remmer, Wolfgang A.  
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes  
; FILE REFERENCE: 1700.0100001  
; CURRENT APPLICATION NUMBER: US/09/733,042  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 60/169,988  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 11282  
; TYPE: DNA  
; ORGANISM: pCvTts  
US-09-733-042-1

Query Match 39.2%; Score 205.2; DB 4; Length 11282;  
Best Local Similarity 98.6%; Pred. No. 9.4e-63;  
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTTAAACATGAGTTAGCAACAT 320  
Db |||  
664 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTTAAACATGAGTTAGCAACAT 723  
QY 321 GCCTTACAG 380  
Db |||  
724 GCCTTACAG 783  
QY 381 CGTGCCTTATTAGGAGGAG 440  
Db |||  
784 CGTGCCTTATTAGGAGGAG 843  
QY 441 CGCATTCGAGAGATATTGTTATTTAAAGTGCC 470  
Db |||  
844 CGCATTCGAGAGATATTGTTATTTAAAGTGCC 873

RESULT 62  
US-08-801-092-5  
; Sequence 5, Application US/08801092  
; Patent No. 6074850  
; GENERAL INFORMATION:  
; APPLICANT: Antelman, Douglas  
; APPLICANT: Gregory, Richard J.  
; APPLICANT: Wils, Kenneth N.  
; TITLE OF INVENTION: Tissue Specific Expression of  
; TITLE OF INVENTION: Retinoblastoma Protein  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/801,092  
; FILING DATE: 14-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/751,517  
; FILING DATE: 15-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 016930-001020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 703-576-0300  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3853 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 209..250  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 254..289  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 293..505  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 509..514  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 518..520  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 524..658  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 662..691  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 695..748  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 752..781  
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 785..829
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1132..1134
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1138..1149
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..862
;
US-08-801-092-5
Query Match      28.9%; Score 151.4; DB 3; Length 3853;
Best Local Similarity 99.3%; Pred. No. 1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 120
Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 200
QY 121 CTGCTTCGGATGTACGGCCAGATATTCGGGT 153
Db 201 CTGCTTCGGATGTACGGCCAGATATATACGGGT 233

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```

RESULT 63
US-09-315-113-5
; Sequence 5, Application US/09315113
; Patent No. 6379927
; GENERAL INFORMATION:
; APPLICANT: Antelman, Douglas
; Gregory, Richard J.
; Wilis, Kenneth N.
; TITLE OF INVENTION: Tissue Specific Expression of
; Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,113
; FILING DATE: 19-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/801,092
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 209..250
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 254..289
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 293..505
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 509..514
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; LOCATION: 518..520
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 524..658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 662..691
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 695..748
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 752..781
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 785..829
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1132..1134
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1138..1149
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..862
;
US-09-315-113-5
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match      28.9%; Score 151.4; DB 4; Length 3853;
Best Local Similarity 99.3%; Pred. No. 1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 120
Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 200
QY 121 CTGCTTCGGATGTACGGCCAGATATTCGGGT 153
Db 201 CTGCTTCGGATGTACGGCCAGATATATACGGGT 233

RESULT 64
US-09-011-745-9
; Sequence 9, Application US/09011745
; Patent No. 6165715
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary KL
; APPLICANT: Weiss, Robin A
; APPLICANT: Takeuchi, Yasuhiro
; APPLICANT: Cosset, Francois-Loic
; TITLE OF INVENTION: Expression systems
; FILE REFERENCE: 09/011,745
; CURRENT APPLICATION NUMBER: US/09/011,745
; CURRENT FILING DATE: 1998-06-22

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; EARLIER APPLICATION NUMBER: PCT/GB96/02061  
 ; EARLIER FILING DATE: 1996-08-23  
 ; EARLIER APPLICATION NUMBER: GB9517263.1  
 ; EARLIER FILING DATE: 1995-08-23  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 3925  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Portion of  
 ; OTHER INFORMATION: construct  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (3910)  
 ; OTHER INFORMATION: n is any nucleotide  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (3911)  
 ; OTHER INFORMATION: n is any nucleotide  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (3912)  
 ; OTHER INFORMATION: n is any nucleotide  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (3913)  
 ; OTHER INFORMATION: n is any nucleotide  
 ; OTHER INFORMATION: n is any nucleotide  
 ; US-09-011-745-9

Query Match 28.9%; Score 151.4; DB 3; Length 3925;  
 Best Local Similarity 99.3%; Pred. No. 1.1e-43;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 70 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 129  
 QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 120  
 Db 130 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 189  
 QY 121 CTGCTCCGCGATGACGGCGCAGATATCGCGT 153  
 Db 190 CTGCTCCGCGATGACGGCGCAGATATCGCGT 222

RESULT 65  
 US-08-801-092-19  
 ; Sequence 19, Application US/08801092  
 ; Patent No. 6074850  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ancelman, Douglas  
 ; APPLICANT: Gregory, Richard J.  
 ; APPLICANT: Wills, Kenneth N.  
 ; TITLE OF INVENTION: Tissue Specific Expression of  
 ; TITLE OF INVENTION: Retinoblastoma Protein  
 ; NUMBER OF SEQUENCES: 46  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: TOWNSEND and TOWNSEND and CREW LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/801,092

; FILING DATE: 14-FEB-1997  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/751,517  
 ; FILING DATE: 15-NOV-1996  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fitts, Renee A.  
 ; REGISTRATION NUMBER: 35,136  
 ; REFERENCE/DOCKET NUMBER: 016930-001020  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-576-0200  
 ; TELEFAX: 703-576-0300  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4026 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 209..250  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 254..289  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 293..505  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 509..514  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 518..520  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 524..658  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 662..691  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 695..748  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 752..781  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 785..829  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 833..862  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1305..1307  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1311..1322  
 ; US-08-801-092-19

Query Match 28.9%; Score 151.4; DB 3; Length 4026;  
 Best Local Similarity 99.3%; Pred. No. 1.1e-43;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 120  
 Db 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGATCTGTTAGGTTAGCGTTTGG 200

Qy 121 CTGCTTCGGCATGTACGGGCCAGATATTCGGGT 153  
Db 201 CTGCTTCGGCATGTACGGGCCAGATATTCGGGT 233

## RESULT 66

US-09-315-113-19  
; Sequence 19, Application US/09315113  
; Patent No. 6379927  
; GENERAL INFORMATION:  
; APPLICANT: Antelman, Douglas  
; Gregory, Richard J.  
; Wills, Kenneth N.  
; TITLE OF INVENTION: Tissue Specific Expression of  
; Retinoblastoma Protein  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/315,113  
; FILING DATE: 19-May-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/801,092  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 016930-001020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 703-576-0300  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4026 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 209..250  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 254..289  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 293..505  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 509..514  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 518..520  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 524..658  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 662..691  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 695..748

; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 752..781  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 785..829  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 833..862  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1305..1307  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1311..1322  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-315-113-19  
  
Query Match . 28.9%; Score 151.4; DB 4; Length 4026;  
Best Local Similarity 99.3%; Pred. No. 1.1e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CTGCTCCCTGCTTGTTGGAGTTCGCTGAGTAGTGCCTGAGGAGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTTGGAGTTCGCTGAGTAGTGCCTGAGGAGCAAAATTAAGCTACA 140  
Qy 61 ACAAGCGAAGGCTTGACCGACAATTGCATGAAGAATCTGCTAGGTTAGCGGTTTGGCG 120  
Db 141 ACAAGCGAAGGCTTGACCGACAATTGCATGAAGAATCTGCTAGGTTAGCGGTTTGGCG 200  
Qy 121 CTGCTTCGGCATGTACGGGCCAGATATTCGGGT 153  
Db 201 CTGCTTCGGCATGTACGGGCCAGATATTCGGGT 233  
  
RESULT 67  
US-08-801-092-33  
; Sequence 33, Application US/08801092  
; Patent No. 6074850  
; GENERAL INFORMATION:  
; APPLICANT: Antelman, Douglas  
; Gregory, Richard J.  
; APPLICANT: Wills, Kenneth N.  
; TITLE OF INVENTION: Tissue Specific Expression of  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/801,092  
; FILING DATE: 14-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/751,517  
; FILING DATE: 15-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 016930-001020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 703-576-0300

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; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 209..250
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 254..289
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 293..505
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 509..514
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 518..520
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 524..658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 662..691
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 695..748
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 752..781
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 785..829
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..862
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1528..1530
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1534..1545
;
US-08-801-092-33

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Query Match      28.9%; Score 151.4; DB 3; Length 4249;
Best Local Similarity 99.3%; Pred No. 1.1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
   |||||||
Db 81 CTGCTCCCTGCTTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 140
   |||||||

QY 61 ACAAGGCAAGGCTTGCACGACATTCATGAGAACTCTAGGTTAGCGCTTTGCG 120
   |||||||
Db 141 ACAAGGCAAGGCTTGCACGACATTCATGAGAACTCTAGGTTAGCGCTTTGCG 200
   |||||||

QY 121 CTGCTTCGCGATGTACGGGCGACATATTCGCGT 153
   |||||||
Db 201 CTGCTTCGCGATGTACGGGCGACATATTCGCGT 233
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RESULT 68
US-09-315-113-33
; Sequence 33, Application US/09315113
; Patent No. 6379927
; GENERAL INFORMATION:
; APPLICANT: Antelman, Douglas
; Gregory, Richard J.
; Wills, Kenneth N.

```

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; TITLE OF INVENTION: Tissue Specific Expression of
; Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/315,113
; FILING DATE: 19-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/801,092
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 209..250
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 254..289
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 293..505
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 509..514
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 518..520
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 524..658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 662..691
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 695..748
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 752..781
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 785..829
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..862
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1528..1530
; FEATURE:

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NAME/KEY: CDS  
LOCATION: 1534..1545  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-315-113-33

Query Match 28.9%; Score 151.4; DB 4; Length 4249;  
Best Local Similarity 99.3%; Pred. No. 1.1e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGACAAATTTAAGCTACA 60  
DB 81 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGGCGGACAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGG 120  
DB 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGG 200  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 153  
DB 201 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 233

RESULT 69  
US-09-311-784A-35  
Sequence 35, Application US/09311784A  
Patent No. 6534482  
GENERAL INFORMATION:  
APPLICANT: Fikes, John D.  
APPLICANT: Hermanson, Gary G.  
APPLICANT: Sette, Alessandro  
APPLICANT: Ishioka, Glenn Y.  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert W.  
APPLICANT: Biimmune Inc.  
TITLE OF INVENTION: Expression Vectors for Stimulating an  
TITLE OF INVENTION: Immune Response and Methods of Using the Same  
FILE REFERENCE: 39963-20022.01  
CURRENT APPLICATION NUMBER: US/09/311,784A  
CURRENT FILING DATE: 1999-05-13  
PRIOR APPLICATION NUMBER: US 60/085,751  
PRIOR FILING DATE: 1998-05-15  
NUMBER OF SEQ ID NOS: 463  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 35  
LENGTH: 5053  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: vector pBP2  
US-09-311-784A-35

Query Match 28.9%; Score 151.4; DB 4; Length 5053;  
Best Local Similarity 99.3%; Pred. No. 1.2e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGGCGGACAAATTTAAGCTACA 60  
DB 81 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGGCGGACAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGG 120  
DB 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGG 200  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 153  
DB 201 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 233

RESULT 70  
US-08-799-569-1  
Sequence 1, Application US/08799569  
Patent No. 6133244  
GENERAL INFORMATION:  
APPLICANT: Michel, Marie-Louise  
TITLE OF INVENTION: Nucleotide Vector, Composition

APPLICANT: Michel, Marie-Louise  
APPLICANT: Mancine, Maryline  
TITLE OF INVENTION: Nucleotide Vector, Composition  
TITLE OF INVENTION: Containing Such Vector, and Vaccine for Immunization  
TITLE OF INVENTION: Against Hepatitis  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegun, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/799,569  
FILING DATE: 12-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/706,337  
FILING DATE: 30-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/633,821  
FILING DATE: 22-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/00483  
FILING DATE: 27-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0128-01000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-799-569-1

Query Match 28.9%; Score 151.4; DB 3; Length 5618;  
Best Local Similarity 99.3%; Pred. No. 1.3e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGGCGGACAAATTTAAGCTACA 60  
DB 81 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGGCGGACAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGG 120  
DB 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGG 200  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 153  
DB 201 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 233

RESULT 71  
US-09-570-546-1  
Sequence 1, Application US/09570546  
Patent No. 6429201  
GENERAL INFORMATION:  
APPLICANT: Michel, Marie-Louise  
TITLE OF INVENTION: Nucleotide Vector, Composition



```

/ Containing Such Vector, and Vaccine for Immunization
/ Against Hepatitis
/
/ NUMBER OF SEQUENCES: 1
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/570,546
/ FILING DATE: 12-May-2000
/ CLASSIFICATION: <Unknown>
/ PRIORITY INFORMATION DATA:
/ APPLICATION NUMBER: US/08/799,569
/ FILING DATE: <unknown>
/ APPLICATION NUMBER: US 08/706,337
/ FILING DATE: 30-AUG-1996
/ APPLICATION NUMBER: US 08/633,821
/ FILING DATE: 22-APR-1996
/ APPLICATION NUMBER: FR 94/00483
/ FILING DATE: 27-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meyers, Kenneth J
/ REGISTRATION NUMBER: 25,146
/ REFERENCE/DOCKET NUMBER: 03495.0128-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 408-4000
/ TELEFAX: (202) 408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5618 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (Genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-570-546-1

Query Match 28.9%; Score 151.4; DB 4; Length 5618;
Best Local Similarity 99.3%; Pred. No. 1.3e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 140
Qy 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGAGATCTGCTTAGGTTAGGCGTTTGG 120
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAGAGATCTGCTTAGGTTAGGCGTTTGG 200
Qy 121 CTGCTCGGATGATGCGGCGCAGATATTCGCGT 153
Db 201 CTGCTCGGATGATGCGGCGCAGATATTCGCGT 233

RESULT 72
US-09-146-072A-1
/ Sequence 1, Application US/09146072A
/ Patent No. 6635624
/ GENERAL INFORMATION:
/ APPLICANT: Davis, Heather L.
/ APPLICANT: Whalen, Robert G.
/ APPLICANT: Michel, Marie-Louise
/ TITLE OF INVENTION: NUCLEOTIDE VECTOR, COMPOSITION CONTAINING SUCH VECTOR AND VACCINE
/ FOR IMMUNIZATION AGAINST HEPATITIS

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/ FILE REFERENCE: C01040.70004. US
/ CURRENT APPLICATION NUMBER: US/09/146,072A
/ CURRENT FILING DATE: 1998-09-02
/ PRIOR APPLICATION NUMBER: US 08/633,821
/ PRIOR FILING DATE: 1996-08-02
/ PRIOR APPLICATION NUMBER: PCT/FR94/000483
/ PRIOR FILING DATE: 1994-04-27
/ PRIOR APPLICATION NUMBER: FR 93/12659
/ PRIOR FILING DATE: 1993-10-22
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 1
/ LENGTH: 5618
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-09-146-072A-1

Query Match 28.9%; Score 151.4; DB 4; Length 5618;
Best Local Similarity 99.3%; Pred. No. 1.3e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 140
Qy 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGAGATCTGCTTAGGTTAGGCGTTTGG 120
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAGAGATCTGCTTAGGTTAGGCGTTTGG 200
Qy 121 CTGCTCGGATGATGCGGCGCAGATATTCGCGT 153
Db 201 CTGCTCGGATGATGCGGCGCAGATATTCGCGT 233

RESULT 73
US-09-439-923-1
/ Sequence 1, Application US/09439923
/ Patent No. 6426208
/ GENERAL INFORMATION:
/ APPLICANT: Emil D. Kakkis
/ APPLICANT: Becky Tanamachi
/ TITLE OF INVENTION: Recombinant Alpha-L-Irononidase, Methods
/ FOR PRODUCING AND PURIFYING THE SAME AND METHODS FOR
/ TREATING DISEASES CAUSED BY DEFICIENCIES THEREOF
/ FILE REFERENCE: 08000051US00
/ CURRENT APPLICATION NUMBER: US/09/439,923
/ CURRENT FILING DATE: 1999-11-12
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 6200
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1558) ... (3516)
US-09-439-923-1

Query Match 28.9%; Score 151.4; DB 4; Length 6200;
Best Local Similarity 99.3%; Pred. No. 1.4e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 140
Qy 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGAGATCTGCTTAGGTTAGGCGTTTGG 120
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAGAGATCTGCTTAGGTTAGGCGTTTGG 200
Qy 121 CTGCTCGGATGATGCGGCGCAGATATTCGCGT 153

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Db 201 CTGCTTCGGGATGTAGCGGCCAGATATACGGCT 233  
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## RESULT 74

US-09-711-205A-1  
; Sequence 1, Application US/09711205A  
; Patent No. 6589971  
; GENERAL INFORMATION:  
; APPLICANT: Emil D. Kakkis  
; APPLICANT: Becky Tanamachi  
; TITLE OF INVENTION: Recombinant Alpha-L-I-duronidase, Methods  
; TITLE OF INVENTION: for Producing and Purifying the Same and Methods for  
; TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof  
; FILE REFERENCE: 0800051US00  
; CURRENT APPLICATION NUMBER: US/09/711,205A  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US/09/439,923  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6200  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1558)...(3516)  
US-09-711-205A-1

Query Match 28.9%; Score 151.4; DB 4; Length 6200;  
Best Local Similarity 99.3%; Pred. No. 1.4e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
|||  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
|||  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
|||  
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 200  
|||  
QY 121 CTGCTTCGGGATGTAGCGGCCAGATATACGGCT 153  
|||  
Db 201 CTGCTTCGGGATGTAGCGGCCAGATATACGGCT 233  
|||

## RESULT 75

US-09-711-205A-1  
; Sequence 1, Application US/09711205A  
; Patent No. 6589971  
; GENERAL INFORMATION:  
; APPLICANT: Emil D. Kakkis  
; APPLICANT: Becky Tanamachi  
; TITLE OF INVENTION: Recombinant Alpha-L-I-duronidase, Methods  
; TITLE OF INVENTION: for Producing and Purifying the Same and Methods for  
; TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof  
; FILE REFERENCE: 0800051US00  
; CURRENT APPLICATION NUMBER: US/09/711,205A  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US/09/439,923  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6200  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1558)...(3516)  
US-09-711-205A-1

Query Match 28.9%; Score 151.4; DB 4; Length 6200;  
Best Local Similarity 99.3%; Pred. No. 1.4e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
|||  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
|||  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
|||  
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 200  
|||  
QY 121 CTGCTTCGGGATGTAGCGGCCAGATATACGGCT 153  
|||  
Db 201 CTGCTTCGGGATGTAGCGGCCAGATATACGGCT 233  
|||

Search completed: March 11, 2004, 11:09:52  
Job time : 105.601 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:24:22 ; Search time 379.636 Seconds  
(without alignments)

5071.893 Million cell updates/sec

Title: US-09-733-368a-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgtccctcgtgtgtgtt.....accacattggtgcacctc 523

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 184079884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Published Applications NA: \*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500.8	95.8	6836	14	US-10-331-329-18
2	500.8	95.8	8902	9	US-09-729-416A-1
3	500.8	95.8	9737	14	US-10-331-329-22
4	500.8	95.8	9737	14	US-10-331-329-23
5	500.8	95.8	9737	14	US-10-331-329-28
6	500.8	95.8	9871	14	US-10-331-329-24
7	500.8	95.8	10060	14	US-10-331-329-25
8	500.8	95.8	11265	14	US-10-185-318-1
9	500.8	95.8	11265	14	US-10-185-799-1
10	430.8	82.4	11600	9	US-09-847-101B-35
11	430.8	82.4	11600	10	US-09-482-682-49
12	430.8	82.4	11600	15	US-10-403-337-42
13	430.8	82.4	11600	15	US-10-351-890-42
14	393	75.1	8238	10	US-09-482-682-50
15	393	75.1	33622	15	US-10-403-337-44

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Sequence 43, Appl  
Sequence 43, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 61, Appl  
Sequence 69, Appl  
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Sequence 36, Appl  
Sequence 16, Appl  
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Sequence 5, Appl  
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Sequence 4, Appl  
Sequence 21, Appl  
Sequence 11, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 29, Appl

89	151.4	28.9	6595	14	US-10-126-764-29	Sequence 29, Appl
90	151.4	28.9	6623	14	US-10-422-934-6	Sequence 6, Appl
91	151.4	28.9	6639	14	US-10-422-934-12	Sequence 12, Appl
92	151.4	28.9	6695	14	US-10-422-934-8	Sequence 8, Appl
93	151.4	28.9	6695	14	US-10-422-934-14	Sequence 14, Appl
94	151.4	28.9	6695	14	US-10-422-934-15	Sequence 15, Appl
95	151.4	28.9	6746	14	US-10-422-934-15	Sequence 5, Appl
96	151.4	28.9	6801	14	US-10-422-934-13	Sequence 13, Appl
97	151.4	28.9	6801	14	US-10-422-934-16	Sequence 16, Appl
98	151.4	28.9	6818	14	US-10-422-934-7	Sequence 7, Appl
99	151.4	28.9	6828	14	US-10-422-934-1	Sequence 1, Appl
100	151.4	28.9	6833	14	US-10-422-934-10	Sequence 10, Appl

## ALIGNMENTS

```

RESULT 1
US-10-331-329-18
/ Sequence 18, Application US/10331329
/ Publication NO. US20030180267A1
/ GENERAL INFORMATION:
/ APPLICANT: HARRINGTON, JOHN J.
/ APPLICANT: SHERF, BRUCE
/ APPLICANT: RUNDLETT, STEPHEN
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
/ TITLE OF INVENTION: ENDOGENOUS GENES
/ FILE REFERENCE: 0221-0003CON
/ CURRENT APPLICATION NUMBER: US/10/331,329
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: 09/276,820
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 09/263,814
/ PRIOR FILING DATE: 1999-03-08
/ PRIOR APPLICATION NUMBER: 09/253,022
/ PRIOR FILING DATE: 1999-02-19
/ PRIOR APPLICATION NUMBER: 09/159,643
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 08/941,223
/ PRIOR FILING DATE: 1997-09-26
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 18
/ LENGTH: 6836
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-331-329-18

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Db	1599	TTACGATGAGTTAGCAACATGCGCTTACAGAGAGAGAAAACGCGCTGCGATGCCGATGG	1658
Qy	361	TGGAAGTAAGGTGTGACATGCTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGA	420
Db	1659	TGGAAGTAAGGTGTGACATGCTGCCTTATTAGGAAGGCAACAGACAGGTCTGACATGGA	1718
Qy	421	TTTGGACGACCACTAAATTCGGATTTGCAGAGAT-AATTGATTAAAGTGGCTAGCTCGAT	479
Db	1719	TTTGGACGACCACTGAATTCGGATTTGCAGAGATTAATTGATTAAAGTGGCTAGCTCGAT	1778
Qy	480	ACAATAAAGCCCATTTGACCATTCACCAATTTGGTGTGCACTC	523
Db	1779	ACAATAAAGCCCATTTTGCACATTCACCAATTTGGTGTGCACTC	1822

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RESULT 2
US-09-729-416A-1
; Sequence 1, Application US/09729416A
; Patent No. US20020055172A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; TITLE OF INVENTION: MULTIPLE PROMOTER EXPRESSION CONSTRUCTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 0221-0004C
; CURRENT APPLICATION NUMBER: US/09/729,416A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8902
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: (PRIG-MPI)
US-09-729-416A-1

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Query Match	95.8%	Score 500.8	DB 14	Length 9737
Best Local Similarity	98.5%	Prod. No. 5.9e-162		
Matches 516	Conservative 0	Mismatches 7	Indels 1	Gaps 1
QY	1	CTGCTCCCTCTGTGTCGTTGGAGGTCGCTCAGTAGTGCGCGAGCAAAATTTAAGCTACA	60	
Db	1152	CTGCTCCCTCTGTGTCGTTGGAGGTCGCTCAGTAGTGCGCGAGCAAAATTTAAGCTACA	1211	
QY	61	ACAGGCGAGGCTTGACGCGAATTCGATGAAGATCTCCTTAGGGTAGGCGGTTTTGCG	120	
Db	1212	ACAGGCGAGGCTTGACGCGAATTCGATGAAGATCTCCTTAGGGTAGGCGGTTTTGCG	1271	
QY	121	CTGCTTCGCGATGTACGGGCGACATATTCGCTATCTGAGGGGACTAGGGCTGTGTTTAGG	180	
Db	1272	CTGCTTCGCGATGTACGGGCGACATATACGGGTATCTGAGGGGACTAGGGCTGTGTTTAGG	1331	
QY	181	CGAAGAGCGGGGCTTCGGTTGTACGGGTTAGAGTCCTCCACGATATAGTAGTTTCGC	240	
Db	1332	CGCCACGCGGGGCTTCGGTTGTACGGGTTAGAGTCCTCCACGATATAGTAGTTTCGC	1391	
QY	241	TTTTGCAATAGGAGGGGGAATGTAGCTTTATGCAATCTCTTGTAGCTCTTGCAACTGG	300	

Db 1392 TTTTCCATAGGAGGGGAAATGAGTCTTATGCATACACTTGTAGTCTTGCACATGG 1451  
 QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCGCATGG 360  
 Db 1452 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCGCATGG 1511  
 QY 361 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
 Db 1512 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 1571  
 QY 421 TTGGACGAACCACTTAATCCGCAATTCAGAGAT-ATTGTATTTAAGTGTAGTCCGAT 479  
 Db 1572 TTGGACGAACCACTTAATCCGCAATTCAGAGAT-ATTGTATTTAAGTGTAGTCCGAT 1631  
 QY 480 ACAATAAGCCGCAATTCAGCAATTCACACATTCGTTGTCACCTC 523  
 Db 1632 ACAATAAGCCGCAATTCAGCAATTCACACATTCGTTGTCACCTC 1675

## RESULT 5

US-10-331-329-28

; Sequence 28, Application US/10331329

; Publication No. US20030180267A1

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERP, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003CON

; CURRENT APPLICATION NUMBER: US/10/331,329

; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 28

; LENGTH: 9737

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8347)

; OTHER INFORMATION: a, c, t, g, other or unknown

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8499)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-10-331-329-28

Query Match

Best Local Similarity 95.8%; Score 500.8; DB 14; Length 9737;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTAGTGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTAGTGTGGCGGAGCAAAATTTAAGCTACA 1211  
 QY 61 ACAAGGCAAGGCTTGACCGACAAATTCGATGAAGATCTGCTTAGGGTTAGCGCTTTTGG 120  
 Db 1212 ACAAGGCAAGGCTTGACCGACAAATTCGATGAAGATCTGCTTAGGGTTAGCGCTTTTGG 1271  
 QY 121 CTGCTCCGATGTAGCGGCGAGATTTCCGGTATCTGAGGCGGAGCTAGGTGTGTAGG 180

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 QY 181 CGAAAGAGGGGGCTTGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTGGC 240  
 Db 1332 CGCCACAGGGGGCTTGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTGGC 1391  
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 Db 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451  
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 Db 1452 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCGCATGG 1511  
 QY 361 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
 Db 1512 TGGAGTAAAGTGTAGTACGATCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 1571  
 QY 421 TTGGACGAACCACTTAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGTAGTCCGAT 479  
 Db 1572 TTGGACGAACCACTTAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGTAGTCCGAT 1631  
 QY 480 ACAATAAGCCGCAATTCAGCAATTCACACATTCGTTGTCACCTC 523  
 Db 1632 ACAATAAGCCGCAATTCAGCAATTCACACATTCGTTGTCACCTC 1675

## RESULT 6

US-10-331-329-24

; Sequence 24, Application US/10331329

; Publication No. US20030180267A1

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERP, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003CON

; CURRENT APPLICATION NUMBER: US/10/331,329

; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 9871

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8481)

; OTHER INFORMATION: a, c, t, g, other or unknown

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8633)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-10-331-329-24

Query Match

Best Local Similarity 95.8%; Score 500.8; DB 14; Length 9871;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTAGTGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 1286 CTGCTCCCTGCTTGTGTGGAGGTGCGTGTAGTGTGGCGGAGCAAAATTTAAGCTACA 1345

QY	61	ACRAGCGAGGCTTGACCGACAAATTGCATCAGAAATCTGCTTAGGGTTAGGCGTTTTCGG	120
Db	1346	ACRAGCGAGGCTTGACCGACAAATTGCATCAGAAATCTGCTTAGGGTTAGGCGTTTTCGG	1405
QY	121	CTGCTTCGCAGTACGGCGCCAGATATTCCGCTATCTAGGGGCACTAGGGTGTGTTTAGG	180
Db	1406	CTGCTTCGCAGTACGGCGCCAGATATACGGCTATCTAGGGGCACTAGGGTGTGTTTAGG	1465
QY	181	CGAAGCGGGGCTTCGGTTACGGGTTAGGAGTCCCTCAGATATAGTAGTTTCGC	240
Db	1466	CSCCAGCGGGGCTTCGGTTACGGGTTAGGAGTCCCTCAGATATAGTAGTTTCGC	1525
QY	241	TTTTCATPAGGAGGGGAAATGTAGTCTTATGCAATCTTTGTAGCTTTCGCAACATGG	300
Db	1526	TTTTCATPAGGAGGGGAAATGTAGTCTTATGCAATACATTTGTAGCTTCGCAACATGG	1585
QY	301	TACCATGAGTTAGCAACATCCCTTACAGGAGAGAAAGCACCGTGCAATCCGATTTGG	360
Db	1586	TACCATGAGTTAGCAACATCCCTTACAGGAGAGAAAGCACCGTGCAATCCGATTTGG	1645
QY	361	TGGAAGTAAAGTGGAACGATCGCTCTTATAGGAGGCAACAGACGGGTCTCATCGGA	420
Db	1646	TGGAAGTAAAGTGGAACGATCGCTCTTATAGGAGGCAACAGACAGGCTCTCATCGGA	1705
QY	421	TTGAGCAAGCAACTAAATTCCGCACTTGCAGAGT-ATTGTATTAAAGTGCGTAGTCGAT	479
Db	1706	TTGAGCAAGCAACTAAATTCCGCACTTGCAGAGTATTGTATTAAAGTGCGTAGTCGAT	1765
QY	480	ACAAATAAGCCATTGTACCAATTCACCAANTGGTGTGCACCTC	523
Db	1766	ACAAATAAGCCATTGTACCAATTCACCAANTGGTGTGCACCTC	1809

Query Match	95.8%;	Score 500.8;	DB 14;	Length 10060;
Best local similarity	98.5%;	Pred. No. 6e-162;		
Matches 516;	Conservative 0;	Mismatches 7;	Indels 1;	Gaps 1;
Qy	1	CTGCTCCCTGCTGTGTGTGTCGAGGTGCGTCAGTAGTCGGCGAGCAAAATTTAAAGCTACA	60	
Db	1475	CTGCTCCCTGCTGTGTGTGTCGAGGTGCGTCAGTAGTCGGCGAGCAAAATTTAAAGCTACA	1534	
Qy	61	ACAAGGCAAGGCTTGACCGCACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGGTTTTGCG	120	
Db	1535	ACAAGGCAAGGCTTGACCGCACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGGTTTTGCG	1594	
Qy	121	CTGCTTGGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTATTAG	180	
Db	1595	CTGCTTGGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTATTAG	1654	
Qy	181	CGAAAAGCGGGGCTTCGCTTCTACGGGTAGGAGTCCCTCAGGATATAGTAGTTTCGC	240	
Db	1655	CGCCACAGGGGGCTTCGCTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC	1714	
Qy	241	TTTTGCATTAGGAGGGGGAATGTAGTCTTATGCAATTACTTTGTGTAGTCTTTGCAACATGG	300	
Db	1715	TTTTGCATTAGGAGGGGGAATGTAGTCTTATGCAATTACTTTGTGTAGTCTTTGCAACATGG	1774	
Qy	301	TACGATGATTAGCAACATGCTTTACAAGGAGAGAAAGCACCGTGATGCGGATGG	360	
Db	1775	TACGATGATTAGCAACATGCTTTACAAGGAGAGAAAGCACCGTGATGCGGATGG	1834	
Qy	361	TGGAGTAGTAGGTGTTACCATGTCGCTTATTTAGGAGGCAACAGACGGGTGTGACATGGA	420	
Db	1835	TGGAGTAGTAGGTGTTACCATGTCGCTTATTTAGGAGGCAACAGACGGGTGTGACATGGA	1894	
Qy	421	TTGGACGAACCACTAAATTCGCATTTGCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT	479	
Db	1995	TTGGACGAACCACTGAATTCGCATTTGCAGAGATTAATTGTATTTAAGTGCCTAGCTCGAT	1954	
Qy	480	ACAATAAACGCCATTTGACCAATTCACCAANTGGTGTGCACTTC	523	
Db	1955	ACAATAAACGCCATTTGACCAATTCACCAANTGGTGTGCACTTC	1998	

1	QY	CTGCTCCCTGCTTGTGTGTGGAGTGTGCTGAGTAGTTCGCGAGCAAAATTTAAGCTACA	60
110	Db	CTGCTCCCTGCTTGTGTGTGGAGTGTGCTGAGTAGTTCGCGAGCAAAATTTAAGCTACA	169
61	QY	ACAAAGCAAGCTTGACCGACAATTCATCAAGAAATCTGCTTAGAGGTAGCGCTTTTGGC	120
170	Db	ACAAAGCAAGCTTGACCGACAATTCATCAAGAAATCTGCTTAGAGGTAGCGCTTTTGGC	229
121	QY	CTGCTTTCGCAGATGACGGGCCAGAAATTCGCTATCTAGAGGGAATGAGGTGTGTTTAGG	189
230	Db	CTGCTTTCGCAGATGACGGGCCAGAAATTCGCTATCTAGAGGGAATGAGGTGTGTTTAGG	289
181	QY	CGAAAGCGGGCTTCGGTGTGACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC	240
290	Db	CGCCACGCGGGGTTTCGGTGTGACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC	349
241	QY	TTTTCGATPAGGAGGGGAAATGTAGTCTTATGCAATACTCTTTAGTCTTTGCAACATGG	300
350	Db	TTTTCGATPAGGAGGGGAAATGTAGTCTTATGCAATACTCTTTAGTCTTTGCAACATGG	409
301	QY	TAAACATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGACCGTGCATGCCGATTCGG	360
410	Db	TAAACATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGACCGTGCATGCCGATTCGG	469
361	QY	TGGAAGTAGGTGGTACGATCGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA	420
470	Db	TGGAAGTAGGTGGTACGATCGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA	529
421	QY	TTTGGACGAACCAATTAATTCGGCATTCGACAGAT--TTTGTATTTAAGTGCCTAGCTCGAT	479
530	Db	TTTGGACGAACCAATTAATTCGGCATTCGACAGATTAATTTATTAGTGCCTAGCTCGAT	589
480	QY	ACAAATAAGCGCATTTGACCAATTCACACATTTGGTGTGCACCTC	523
590	Db	ACAAATAAGCGCATTTGACCAATTCACACATTTGGTGTGCACCTC	633

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RESULT 9
US-10-185-799-1
; Sequence 1, Application US/10185799
; Publication No. US2003007242A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, JEFFREY S.
; APPLICANT: BRADY, JAMIE L.
; APPLICANT: LEW, ANDREW M.
; TITLE OF INVENTION: ENHANCEMENT OF IMMUNE RESPONSE USING TARGETING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: FBRC:0090USC1
; CURRENT APPLICATION NUMBER: US/10/185,799
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/402,020
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: PCT/AU98/00208
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: AU PP5891
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: AU PP1830
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11265
; TYPE: DNA
; ORGANISM: Murine
US-10-185-799-1

```

Qy	61	ACAAGCGAAGGCTTGACCGACAATTCGCATGAAGAATCTGCTTAGGGTTAGCGCTTTTCGC	120
Db	170	ACAAGCGAAGGCTTGACCGACAATTCGCATGAAGAATCTGCTTAGGGTTAGCGCTTTTCGC	229
Qy	121	CTGCTTTCCGATGCTACGGCGCCAGATATTCGCGGTATCTGAGGGGCACTAGGCTGTGTTTAGG	180
Db	230	CTGCTTTCCGATGCTACGGGCCCAATATACGGGTATCTGAGGGGCACTAGGCTGTGTTTAGG	289
Qy	181	CGAAAAGCGGGGCTTCGGTTGTGTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC	240
Db	290	CGCCACAGCGGGGCTTCGGTTGTGTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC	349
Qy	241	TTTTCGATAGGAGGGGGAATGTAGTCTTATGCAATACTCTCTGTAGTCTTGCACATCG	300
Db	350	TTTTCGATAGGAGGGGGAATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATCG	409
Qy	301	TAAACATGAGTTAGCAACAATGCCCTTACAAGCAGAGAAAAGCACCGTGCAATGCCATGG	360
Db	410	TAAACATGAGTTAGCAACAATGCCCTTACAAGCAGAGAAAAGCACCGTGCAATGCCATGG	469
Qy	361	TGGAGTAGTAAGTGCTTACGATCGTGCCTTATTAGGAGGGCAACAGACGGGCTCTGACATGA	420
Db	470	TGGAAGTAGTAAGTGCTTACGATCGTGCCTTATTAGGAGGGCAACAGACGGCTCTGACATGA	529
Qy	421	TTTGGACGAACCACTAAATTCGCGCATTTGCAGAGAT-ATTGTATTTTAAGTGGCTAGTCCGAT	479
Db	530	TTTGGACGAACCACTAAATTCGCGCATTTGCAGAGATATTGTATTTTAAGTGGCTAGTCCGAT	589
Qy	480	ACAAATAACGCCATTGTGACCAATTCACCAATTGGTGTGCACCTC	523
Db	590	ACAAATAACGCCATTGTGACCAATTCACCAATTGGTGTGCACCTC	633

RESULT 10  
US-09-847-101B-35  
Sequence 35, Application US/09847101B  
Publication No. US20020193327A1  
GENERAL INFORMATION:  
APPLICANT: VON SEGGERN, DANIEL  
APPLICANT: NEMEROW, GLEN R.  
APPLICANT: FRIEDLANDER, MARTIN  
TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GEN  
FILE REFERENCE: 229C08-1226B  
CURRENT APPLICATION NUMBER: US/09/847,101B  
CURRENT FILING DATE: 2001-05-01  
PRIOR APPLICATION NUMBER: 09/562,934  
PRIOR FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 35  
LENGTH: 11600  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
US-09-847-101B-35  
OTHER INFORMATION: Description of Artificial Sequence: plasmid MMTV-E2a-SV4

Query Match	95.8%	Score 500.8	DB 14	Length 12657
Best Local Similarity	98.5%	Pred. No. 6.4e-163		
Matches 516	Conservative 0	Mismatches 7	Indels 1	Gaps 1
QY	CTCTCCCTGCTGTGTGTGTGAGGTGCGTGTAGTTCGGCGAGCAAAATTTAAAGTACA 60			
Db	CTGCTCCCTGCTGTGTGTGTGAGGTGCGTGTAGTTCGGCGAGCAAAATTTAAAGTACA 169			



QY 181 CGAAGAGGGGGCTTCGGTGTACGCGTTAGGAGTCCCTCAGCATATAGTATTGGC 240  
Db 11347 CGAAGAGGGGGCTTCGGTGTACGCGTTAGGAGTCCCTCAGCATATAGTATTGGC 11406  
QY 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 11466  
QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGACCGGTGCAATGCCATGG 360  
Db 11467 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGACCGGTGCAATGCCATGG 11526  
QY 361 TGGAGTAAGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
Db 11527 TGGAGTAAGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 11586  
QY 421 TTGGAGCAACCACT 434  
Db 11587 TTGGAGCAACCACT 11600  
RESULT 11  
US-09-482-682-49  
; Sequence 49, Application US/09482682  
; Publication No. US20030157688A1  
; GENERAL INFORMATION:  
; APPLICANT: VON SEGGERN, DANIEL  
; APPLICANT: NEMEROW, GLEN R.  
; APPLICANT: HALLENBECK, PAUL  
; APPLICANT: STEVENSON, SUSAN  
; APPLICANT: SKRIPCHENKO, YELENA  
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,  
; FILE REFERENCE: 1294.0010001  
; CURRENT FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 11600  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: plasmid  
US-09-482-682-49  
Query Match 82.4%; Score 430.8; DB 10; Length 11600;  
Best Local Similarity 99.5%; Pred. No. 1.2e-137;  
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 11167 CTGCTCCCTGCTGTGTGGAGTGGCTGAGTGTAGTGGGAGCAAAATTTAAGCTACA 60  
Db 11167 CTGCTCCCTGCTGTGTGGAGTGGCTGAGTGTAGTGGGAGCAAAATTTAAGCTACA 11226  
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
Db 11227 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 11286  
QY 121 CTGCTTCGGATGTACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTATTAGG 180  
Db 11287 CTGCTTCGGATGTACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTATTAGG 11346  
QY 181 CGAAGAGCGGGCTTCGGTGTACGCGTTAGGAGTCCCTCAGCATATAGTATTGGC 240  
Db 11347 CGAAGAGCGGGCTTCGGTGTACGCGTTAGGAGTCCCTCAGCATATAGTATTGGC 11406  
QY 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 11466  
QY 301 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 360  
Db 11407 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 11466  
QY 361 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGACCGGTGCAATGCCATGG 360

Db 11467 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGACCGGTGCAATGCCATGG 11526  
QY 361 TGGAGTAAGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
Db 11527 TGGAGTAAGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 11586  
QY 421 TTGGAGCAACCACT 434  
Db 11587 TTGGAGCAACCACT 11600  
RESULT 12  
US-10-403-337-42  
; Sequence 42, Application US/10403337  
; Publication No. US20030215948A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Nemerow, Glen R.  
; APPLICANT: Smith, Theodore  
; APPLICANT: Stevenson, Susan C.  
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
; FILE REFERENCE: 22908-1236B  
; CURRENT APPLICATION NUMBER: US/10/403.337  
; CURRENT FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: 10/351,890  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/350,388  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/391,967  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patent In version 3.0  
; SEQ ID NO 42  
; LENGTH: 11600  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo  
US-10-403-337-42  
Query Match 82.4%; Score 430.8; DB 15; Length 11600;  
Best Local Similarity 99.5%; Pred. No. 1.2e-137;  
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 11167 CTGCTCCCTGCTGTGTGGAGTGGCTGAGTGTAGTGGGAGCAAAATTTAAGCTACA 60  
Db 11167 CTGCTCCCTGCTGTGTGGAGTGGCTGAGTGTAGTGGGAGCAAAATTTAAGCTACA 11226  
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
Db 11227 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 11286  
QY 121 CTGCTTCGGATGTACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTATTAGG 180  
Db 11287 CTGCTTCGGATGTACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTATTAGG 11346  
QY 181 CGAAGAGCGGGCTTCGGTGTACGCGTTAGGAGTCCCTCAGCATATAGTATTGGC 240  
Db 11347 CGAAGAGCGGGCTTCGGTGTACGCGTTAGGAGTCCCTCAGCATATAGTATTGGC 11406  
QY 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 11466  
QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGACCGGTGCAATGCCATGG 360  
Db 11467 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGACCGGTGCAATGCCATGG 11526  
QY 361 TGGAGTAAGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
Db 11527 TGGAGTAAGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 11586  
QY 421 TTGGAGCAACCACT 434

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Db      11587 TTGACGACCACT 11600
|||||
RESULT 13
US-10-351-890-42
; Sequence 42, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo
US-10-351-890-42

Query Match      82.4%; Score 430.8; DB 15; Length 11600;
Best Local Similarity 99.5%; Pred. No. 1.2e-137;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGTACA 60
Db      11167 CTGCTCCCTGCTTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGTACA 11226

QY      61 ACHAGGCAAGCTTACCGGCAATTTGATGAAGATCTCTTAGGGTTAGCGTTTTCG 120
Db      11227 ACAAGGCAAGCTTACCGGCAATTTGATGAAGATCTCTTAGGGTTAGCGTTTTCG 11286

QY      121 CTGCTTCGCGATGTACGGGCGAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db      11287 CTGCTTCGCGATGTACGGGCGAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 11346

QY      181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240
Db      11347 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 11406

QY      241 TTTTGCATAGGAGGAGGGAATGCTAGTCTTATGCAATCTCTTGCTTGTCTGCAATGG 300
Db      11407 TTTTGCATAGGAGGAGGGAATGCTAGTCTTATGCAATCTCTTGCTTGTCTGCAATGG 11466

QY      301 TAACCATGATGTAGCAATGCTTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGG 360
Db      11467 TAACGATGTTAGCAATGCTTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGG 11526

QY      361 TGAAGTAAAGTGTGATCGTGTGCTTATTAGGAGGCAACAGCGGGTCTGACATGGA 420
Db      11527 TGAAGTAAAGTGTGATCGTGTGCTTATTAGGAGGCAACAGCGGGTCTGACATGGA 11586

QY      421 TTGAGCAACCACT 434
Db      11587 TTGAGCAACCACT 11600

RESULT 14
US-09-482-682-50
; Sequence 50, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:

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; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 8238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-50

Query Match      75.1%; Score 393; DB 10; Length 8238;
Best Local Similarity 98.8%; Pred. No. 1.2e-124;
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      123 GCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGGCG 182
Db      404 GCGCCCCGATGTACGGGCGAGATATACCGCTATCTGAGGGGACTAGGGTGTGTTAGGCG 463

QY      183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242
Db      464 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 523

QY      243 TTCCATAGGAGGAGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCAATGTA 302
Db      524 TTGCATAGGAGGAGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCAATGTA 583

QY      303 ACGATGAGTTAGCAACTGCTTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTTGGT 362
Db      584 ACGATGAGTTAGCAACTGCTTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTTGGT 643

QY      363 GAAGTAAGTGTGTAGTCTGCTGCTTATTAGGAGGCAACAGCGGGTCTGCAATGAT 422
Db      644 GAAGTAAGTGTGTAGTCTGCTGCTTATTAGGAGGCAACAGCGGGTCTGCAATGAT 703

QY      423 GAGACGACCACTAAATTCGCAATTCGAGATATTTAAGTGCTAGCTCGATACA 482
Db      704 GAGACGACCACTAAATTCGCAATTCGAGATATTTAAGTGCTAGCTCGATACA 763

QY      483 ATAAAGCCATTTGACCACTTCCACATTTGGTGTGACCTC 523
Db      764 ATAAAGCCATTTGACCACTTCCACATTTGGTGTGACCTC 804

RESULT 15
US-10-403-337-44
; Sequence 44, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72

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; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 33622  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid Av3nBg  
US-10-403-337-44

Query Match 75.1%; Score 393; DB 15; Length 33622;  
Best Local Similarity 98.8%; Pred. No. 2.5e-124;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 123 GCTTCGCATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
DB 396 GCGCCCCGATGTACGGGCCAGATATACCGGTAICTGAGGGGACTAGGGTGTGTTAGGCG 455  
  
QY 183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
DB 456 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 515  
  
QY 243 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 302  
DB 516 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 575  
  
QY 303 ACCATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCCTGCGATCGGATGGTG 362  
DB 576 ACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCCTGCGATCGGATGGTG 635  
  
QY 363 GAAGTAAAGTGGTACGATCGTTCCTTATAGGAAGGCAACAGACGGGCTGACATGGATT 422  
DB 636 GAAGTAAAGTGGTACGATCGTTCCTTATAGGAAGGCAACAGACGGGCTGACATGGATT 695  
  
QY 423 GGACGAACCACTAAATTCGCAATTCACCACTTCCACATTTGGTGTGCACCTC 523  
DB 696 GGACGAACCACTAAATTCGCAATTCACCACTTCCACATTTGGTGTGCACCTC 755  
  
QY 483 ATAAAGCGCAATTTGACCACTTCCACATTTGGTGTGCACCTC 523  
DB 756 ATAAAGCGCAATTTGACCACTTCCACATTTGGTGTGCACCTC 796

RESULT 16  
US-10-351-890-44  
; Sequence 44, Application US/10351890  
; Publication No. US2004002060A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Nemerow, Susan C.  
; APPLICANT: Smith, Theodore  
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
; FILE REFERENCE: 22908-1236  
; CURRENT APPLICATION NUMBER: US/10/351,890  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 60/350,388  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/391,967  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 33622  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid Av3nBg  
US-10-351-890-44

Query Match 75.1%; Score 393; DB 15; Length 33622;  
Best Local Similarity 98.8%; Pred. No. 2.5e-124;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGCATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
DB 396 GCGCCCCGATGTACGGGCCAGATATACCGGTAICTGAGGGGACTAGGGTGTGTTAGGCG 455  
  
QY 183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
DB 456 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 515  
  
QY 243 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 302  
DB 516 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 575  
  
QY 303 ACCATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCCTGCGATCGGATGGTG 362  
DB 576 ACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCACCCTGCGATCGGATGGTG 635  
  
QY 363 GAAGTAAAGTGGTACGATCGTTCCTTATAGGAAGGCAACAGACGGGCTGACATGGATT 422  
DB 636 GAAGTAAAGTGGTACGATCGTTCCTTATAGGAAGGCAACAGACGGGCTGACATGGATT 695  
  
QY 423 GGACGAACCACTAAATTCGCAATTCACCACTTCCACATTTGGTGTGCACCTC 523  
DB 696 GGACGAACCACTAAATTCGCAATTCACCACTTCCACATTTGGTGTGCACCTC 755  
  
QY 483 ATAAAGCGCAATTTGACCACTTCCACATTTGGTGTGCACCTC 523  
DB 756 ATAAAGCGCAATTTGACCACTTCCACATTTGGTGTGCACCTC 796

RESULT 17  
US-10-403-337-43  
; Sequence 43, Application US/10403337  
; Publication No. US20030215948A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Nemerow, Glen R.  
; APPLICANT: Smith, Theodore  
; APPLICANT: Stevenson, Susan C.  
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
; FILE REFERENCE: 22908-1236B  
; CURRENT APPLICATION NUMBER: US/10/403,337  
; CURRENT FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: 10/351,890  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/350,388  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/391,967  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 43  
; LENGTH: 35211  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid AvinBg  
US-10-403-337-43

Query Match 75.1%; Score 393; DB 15; Length 35211;  
Best Local Similarity 98.8%; Pred. No. 2.6e-124;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 123 GCTTCGCATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
DB 510 GCGCCCCGATGTACGGGCCAGATATACCGGTAICTGAGGGGACTAGGGTGTGTTAGGCG 569  
  
QY 183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
DB 570 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 629  
  
QY 243 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 302  
DB 630 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 689

QY 303 ACGATGAGTTAGCAACATCCCTTACAGGAGAGAAAGAACCCCTGCATGCCGATTTGGT 362  
Db 690 ACGATGAGTTAGCAACATCCCTTACAGGAGAGAAAGAACCCCTGCATGCCGATTTGGT 749  
QY 363 GAAGTAGGTTGATACATCGTCCCTTATTAGGAAGGCAACAGACGGGTCTGCATGGATT 422  
Db 750 GAAGTAGGTTGATACATCGTCCCTTATTAGGAAGGCAACAGACGGGTCTGCATGGATT 809  
QY 423 GGACCAACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAAGTGCCTAGCTCGATACA 482  
Db 810 GGACCAACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAAGTGCCTAGCTCGATACA 869  
QY 483 ATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 870 ATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCACCTC 910

RESULT 18  
US-10-351-890-43  
; Sequence 43, Application US/10351890  
; Publication No. US20040002060A1  
; GENERAL INFORMATION:  
; APPLICANT: Stevenson, Susan C.  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Smith, Theodore  
; APPLICANT: Nemerow, Glen R.  
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
; FILE REFERENCE: 22508-1236  
; CURRENT APPLICATION NUMBER: US/10/351,890  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 60/350,388  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/391,967  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 43  
; LENGTH: 35211  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid AvinBg  
US-10-351-890-43

Query Match 75.1%; Score 393; DB 15; Length 35211;  
Best Local Similarity 98.8%; Pred. No. 2.6e-124;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGGATGTAGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
Db 510 GCGCCCCGATGTAGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 569  
QY 183 AAAACGGGGCTTCGGTTGATAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
Db 570 AAAACGGGGCTTCGGTTGATAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 629  
QY 243 TTGCATAGGGAGGGGAAATGATGCTTTATGCAATCTTTGTAGTCTTGCAACATGTA 302  
Db 630 TTGCATAGGGAGGGGAAATGATGCTTTATGCAATCTTTGTAGTCTTGCAACATGTA 689  
QY 303 ACGTAGTTAGCAACATGCCCTTACAGGAGAGAAAGAACCCCTGCATGCCGATTTGGT 362  
Db 690 ACGTAGTTAGCAACATGCCCTTACAGGAGAGAAAGAACCCCTGCATGCCGATTTGGT 749  
QY 363 GAAGTAGGTTGATACATCGTCCCTTATTAGGAAGGCAACAGACGGGTCTGCATGGATT 422  
Db 750 GAAGTAGGTTGATACATCGTCCCTTATTAGGAAGGCAACAGACGGGTCTGCATGGATT 809  
QY 423 GGACCAACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAAGTGCCTAGCTCGATACA 482  
Db 810 GGACCAACCACTAAATTCGCAATTCGAGAGATATTGTATTTAAAGTGCCTAGCTCGATACA 869

QY 483 ATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 870 ATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCACCTC 910

RESULT 19  
US-09-897-006-9  
; Sequence 9, Application US/09897006  
; Patent No. US20020106729A1  
; GENERAL INFORMATION:  
; APPLICANT: Bleck, Gregory  
; TITLE OF INVENTION: Expression Vectors  
; FILE REFERENCE: GALA-06415  
; CURRENT APPLICATION NUMBER: US/09/897,006  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/215,851  
; PRIOR FILING DATE: 2000-07-03  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 5130  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-897-006-9

Query Match 52.8%; Score 276.2; DB 9; Length 5130;  
Best Local Similarity 93.7%; Pred. No. 2.7e-84;  
Matches 310; Conservative 0; Mismatches 18; Indels 3; Gaps 2;

QY 195 TCGGTTGACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGGAG 254  
Db 2260 TAGGGTGTGCTGCCAACTGCATCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGGAG 2319  
QY 255 GGGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGTTAAACGATGAGTTAG 314  
Db 2320 GGGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGTTAAACGATGAGTTAG 2379  
QY 315 CAACTGCTCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGGTGG 374  
Db 2380 CAACTGCTCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGGTGG 2439  
QY 375 TAGCATCGTGCCTTTATTAGGAAGGCAACAGACGGGTCTGCATGATTTGACGCAACT 434  
Db 2440 TAGCATCGTGCCTTTATTAGGAAGGCAACAGACGGGTCTGCATGATTTGACGCAACT 2499  
QY 435 AAATTCCGCTTGCAGAGAT-ATTGCTATTAAAGTGCCTAGCTCGATACAATAAAGCCCA- 492  
Db 2500 GAATTCCGCTTGCAGAGAT-ATTGCTATTAAAGTGCCTAGCTCGATACAATAAAGCCCA- 2559  
QY 493 -TTTGACCAATTCACCAATTTGGTGTGCACCT 522  
Db 2560 TTTTGACCAATTCACCAATTTGGTGTGCACCT 2590

RESULT 20  
US-09-897-511A-9  
; Sequence 9, Application US/09897511A  
; Publication No. US2003009282A1  
; GENERAL INFORMATION:  
; APPLICANT: Bremel, Robert  
; APPLICANT: Miller, Linda  
; APPLICANT: Bleck, Gregory  
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors  
; FILE REFERENCE: GALA-06416  
; CURRENT APPLICATION NUMBER: US/09/897,511A  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/215,925  
; PRIOR FILING DATE: 2000-07-03  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9

```
/ LENGTH: 5130
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-09-897-51A-9

Query Match          52.8%; Score 276.2; DB 10; Length 5130;
Best Local Similarity 93.7%; Pred. No. 2.2e-84;
Matches 310; Conservative 0; Mismatches 18; Indels 3; Gaps 2;

QY 195 TCGTTGACCGGTAGGAGTCCCTCAGGATATAGTATGTTTCGCTTTGTCATAGGAG 254
Db 2260 TAGGGTGTCTGCAACTGCATCCCTCAGGATATAGTATGTTTCGCTTTGTCATAGGAG 2319
QY 255 GGGGAATGTAGTCTTATCACTCTTGTAGTCTTGCAACATGTTAGCATGTTAG 314
Db 2320 GGGGAATGTAGTCTTATCACTCTTGTAGTCTTGCAACATGTTAGCATGTTAG 2379
QY 315 CAACATGCTTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGG 374
Db 2380 CAACATGCTTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGG 2439
QY 375 TAGCATCTGCTTTATAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCAACT 434
Db 2440 TAGCATCTGCTTTATAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCAACT 2499
QY 435 AAATTCGCATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATATAACGCCA- 492
Db 2500 GAATTCGCATTCAGAGATATTGTATTTAAGTGCCTAGCTCGATACATATAACGCCA- 2559
QY 493 -TTTGACCATTCACCATTTGTTGCACT 522
Db 2560 TTTTGACCATTCACCATTTGTTGCACT 2590

RESULT 21
US-09-965-703-69
/ Sequence 69, Application US/09965703
/ Patent No. US20020119521A1
/ GENERAL INFORMATION:
/ APPLICANT: Rohm and Haas Company
/ APPLICANT: Palli, Subba Reddy
/ APPLICANT: Kapitskaya, Marianna Zinovjevna
/ APPLICANT: Cress, Dean Ervin
/ TITLE OF INVENTION: No. US20020119521A1el Bcdysone Receptor-Based Inducible Gene Expre
/ FILE REFERENCE: A01020B
/ CURRENT APPLICATION NUMBER: US/09/965,703
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR FILING DATE: 2001-03-21
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 69
/ LENGTH: 262
/ TYPE: DNA
/ ORGANISM: Rous sarcoma virus
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: No. US20020119521A1el Sequence
US-09-965-703-69

Query Match          49.2%; Score 257.2; DB 9; Length 262;
Best Local Similarity 98.9%; Pred. No. 2.2e-78;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATCTCTTTGTAGTCTTGCAACATGTTAGTGAAGTAAGTGGTACGAT 320
Db 1 ATGTAGTCTTATGCAATCTCTTTGTAGTCTTGCAACATGTTAGTGAAGTAAGTGGTACGAT 60

QY 321 GCCTTACAAAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGAT 380
Db 61 GCCTTACAAAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGAT 120
QY 381 CGTGCCTTTATTAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCACTAAATTC 440
Db 121 CGTGCCTTTATTAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCACTAAATTC 180
QY 441 CGCATTCGACAGATATTGTATTTAAGTGCCTAGCTCGATACATAAAGCGCATTTTGACCA 500
Db 181 CGCATTCGACAGATATTGTATTTAAGTGCCTAGCTCGATACATAAAGCGCATTTTGACCA 240
QY 501 TTCAACCATTTGGTGTGCACCT 522
Db 241 TTCAACCATTTGGTGTGCACCT 262

US-09-965-703-69

Query Match          49.2%; Score 257.2; DB 9; Length 262;
Best Local Similarity 98.9%; Pred. No. 2.2e-78;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATCTCTTTGTAGTCTTGCAACATGTTAGTGAAGTAAGTGGTACGAT 320
Db 1 ATGTAGTCTTATGCAATCTCTTTGTAGTCTTGCAACATGTTAGTGAAGTAAGTGGTACGAT 60
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QY 321 GCCTTACAAAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGAT 380
Db 61 GCCTTACAAAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGAT 120
QY 381 CGTGCCTTTATTAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCACTAAATTC 440
Db 121 CGTGCCTTTATTAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCACTAAATTC 180
QY 441 CGCATTCGACAGATATTGTATTTAAGTGCCTAGCTCGATACATAAAGCGCATTTTGACCA 500
Db 181 CGCATTCGACAGATATTGTATTTAAGTGCCTAGCTCGATACATAAAGCGCATTTTGACCA 240
QY 501 TTCAACCATTTGGTGTGCACCT 522
Db 241 TTCAACCATTTGGTGTGCACCT 262

RESULT 22
US-10-239-134-61
/ Sequence 61, Application US/10239134
/ Publication No. US20040033600A1
/ GENERAL INFORMATION:
/ APPLICANT: Rohm and Haas Company
/ APPLICANT: Palli, Subba Reddy
/ APPLICANT: Kapitskaya, Marianna Zinovjevna
/ APPLICANT: Cress, Dean Ervin
/ TITLE OF INVENTION: No. US20040033600A1el Bcdysone Receptor-Based Inducible Gene Expre
/ FILE REFERENCE: RH0020
/ CURRENT APPLICATION NUMBER: US/10/239,134
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR FILING DATE: 2001-02-20
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 61
/ LENGTH: 262
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: No. US20040033600A1el Sequence
US-10-239-134-61

Query Match          49.2%; Score 257.2; DB 12; Length 262;
Best Local Similarity 98.9%; Pred. No. 2.2e-78;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATCTCTTTGTAGTCTTGCAACATGTTAGTGAAGTAAGTGGTACGAT 320
Db 1 ATGTAGTCTTATGCAATCTCTTTGTAGTCTTGCAACATGTTAGTGAAGTAAGTGGTACGAT 60

QY 321 GCCTTACAAAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGAT 380
Db 61 GCCTTACAAAGGAGAGAAAAGCAGCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGAT 120
QY 381 CGTGCCTTTATTAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCACTAAATTC 440
Db 121 CGTGCCTTTATTAGGAGGCAAGCAGCGGTCTGCAATGATTTGACGACCACTAAATTC 180
QY 441 CGCATTCGACAGATATTGTATTTAAGTGCCTAGCTCGATACATAAAGCGCATTTTGACCA 500
Db 181 CGCATTCGACAGATATTGTATTTAAGTGCCTAGCTCGATACATAAAGCGCATTTTGACCA 240
QY 501 TTCAACCATTTGGTGTGCACCT 522
Db 241 TTCAACCATTTGGTGTGCACCT 262

RESULT 23
US-10-155-736A-1
```

```
; Sequence 1, Application US/10155736A
; Publication No. US20030095948A1
; GENERAL INFORMATION:
; APPLICANT: Universit. di Torino
; TITLE OF INVENTION: Vector and methods of use for selective expression of genes in si
; FILE REFERENCE: 36019/MMN
; CURRENT APPLICATION NUMBER: US/10/155,736A
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: -
; SEQ ID NO 1
; LENGTH: 10469
; TYPE: DNA
; ORGANISM: HIV-1
US-10-155-736A-1

Query Match 41.6%; Score 217.4; DB 14; Length 10469;
Best Local Similarity 99.1%; Pred. No. 9.4e-64;
Matches 229; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 260 AATGTAGTCTTATGCAATATCTCTTGTAGTCTTGCACATGTTAAGCATGTTAGCAACA 319
DB 2218 AATGTAGTCTTATGCAATATCTCTTGTAGTCTTGCACATGTTAAGCATGTTAGCAACA 2277

QY 320 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTGGTGAACA 379
DB 2278 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTGGTGAACA 2337

QY 380 TCGTGCCTTATTAGGAGGCAACAGACGCGTCTGACATGATGAGTGAACCACTAAATT 439
DB 2338 TCGTGCCTTATTAGGAGGCAACAGACGCGTCTGACATGATGAGTGAACCACTAAATT 2397

QY 440 -CGCATTCGACAGATATCTTATTAAGTGCCTAGCTCCGATACATAAAGC 489
DB 2398 GCCGCATTGACAGATATCTTATTAAGTGCCTAGCTCCGATACATAAAGC 2448

RESULT 24
US-09-733-042-1
; Sequence 1, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: pcYtts
US-09-733-042-1

Query Match 39.2%; Score 205.2; DB 9; Length 11282;
Best Local Similarity 98.6%; Pred. No. 1.6e-59;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGTTAAGCATGTTAGCAACAT 320
DB 664 ATCCAGTCTTATGCAATATCTTGTAGTCTTGCACATGTTAAGCATGTTAGCAACAT 723

QY 321 GCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAAGTGAACAT 380
DB 724 GCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAAGTGAACAT 783

QY 381 CGTGCCTTATTAGGAGGCAACAGACGCGTCTGACATGATGGAACCACTAAATT 440
DB 784 CGTGCCTTATTAGGAGGCAACAGACGCGTCTGACATGATGGAACCACTAAATT 843

QY 441 CGCATTCGACAGATATCTTATTAAGTGCCTAGTCCGATGTTAGTGCCTAGTCCGAT 470
DB 844 CGCATTCGACAGATATCTTATTAAGTGCCTAGTCCGATGTTAGTGCCTAGTCCGAT 873

RESULT 26
US-09-921-143-36
; Sequence 36, Application US/09921143
; Publication No. US20030215921A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: EF112P6
; CURRENT APPLICATION NUMBER: US/09/921,143
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/223,276
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 36
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-921-143-36
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Query Match 35.9%; Score 187.6; DB 11; Length 5283;  
 Best Local Similarity 91.5%; Pred. No. 1.4e-53;  
 Matches 214; Conservative 0; Mismatches 9; Indels 11; Gaps 1;  
 QY 300 GTAACGATGATGACCAATGCTTTAAGGAGAGAAAAAGCAACCGTGCATGCCGATTG 359  
 DB 252 GTACGGTGTAGTACCAATGCTTTAAGGAGAGAAAAAGCAACCGTGCATGCCGATTG 311  
 QY 360 GTGGAAGTAG-----GTGTACGATGCTGCTTTATTAGGAAGGCAACGAGCG 408  
 DB 312 GTGGGAGTAGGTTGATGATGGTATGATGCTGCTTTATTAGGAAGGCAACGAGCG 371  
 QY 409 GTCTGACATGATGACCAACCACTAAATTCGCAATTCAGAGATATTTTAAGTG 468  
 DB 372 GTCTAACGAGTTGACGACCACTGAATTCGCAATTCAGAGATATTTTAAGTG 431  
 QY 469 CCTAGCTGATACAAATAAGCCATTTGACCAATCACCATTGGTGTGCACCT 522  
 DB 432 CCCAGCTGATACAAATAAGCCATTTGACCAATCACCATTGGTGTGCACCT 485

## RESULT 27

US-10-182-327-16  
 ; Sequence 16, Application US/10182327  
 ; Publication No. US20040043468A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
 ; APPLICANT: THE NEUROSCIENCE INSTITUTE  
 ; APPLICANT: MAURO, Vincent P.  
 ; APPLICANT: EDELMAN, Gerald M.  
 ; APPLICANT: CHAPPELL, Stephen A.  
 ; APPLICANT: OWENS, Geoffrey  
 ; APPLICANT: PINKSTAFF, Jason K.  
 ; APPLICANT: KRUSHEL, Leslie  
 ; APPLICANT: ZHOU, Wei  
 ; TITLE OF INVENTION: SYNTHETIC INTERNAL RIBOSOME ENTRY SITES AND METHODS OF IDENTIFYING  
 ; FILE REFERENCE: SCRIPI360-1  
 ; CURRENT APPLICATION NUMBER: US/10/182,327  
 ; CURRENT FILING DATE: 2002-12-03  
 ; PRIOR APPLICATION NUMBER: PCT/US 01/02586  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: US 60/261,312  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: US 60/230,956  
 ; PRIOR FILING DATE: 2000-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/230,852  
 ; PRIOR FILING DATE: 2000-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/207,804  
 ; PRIOR FILING DATE: 2000-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/186,496  
 ; PRIOR FILING DATE: 2000-03-02  
 ; PRIOR APPLICATION NUMBER: US 60/178,816  
 ; NUMBER OF SEQ ID NOS: 197  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 16  
 ; LENGTH: 6250  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: VECTOR  
 US-10-182-327-16

Query Match 33.5%; Score 175.2; DB 12; Length 6250;  
 Best Local Similarity 98.3%; Pred. No. 3e-49;  
 Matches 177; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 259 AAATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGATTAGCAAC 318  
 DB 3164 AAATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGATTAGCAAC 3223  
 QY 319 ATGCTTACAGGAGAGAAAAAGCAACCGTGCATGCCGATTGGTGAAGTAAGGTGGTAGC 378

DB 3224 ATGCTTACAGGAGAGAAAAAGCAACCGTGCATGCCGATTGGTGAAGTAAGGTGGTAGC 3283  
 QY 379 ATGCTGCTTATTAGGAAGGCAACGAGCGGTCTGACATGGATTGGACGAACCACTAAAT 438  
 DB 3284 ATGCTGCTTATTAGGAAGGCAACGAGCGGTCTGACATGGATTGGACGAACCACTAGAT 3343

## RESULT 28

US-10-182-329-109  
 ; Sequence 109, Application US/10182329  
 ; Publication No. US20040005564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
 ; APPLICANT: MAURO, Vincent P.  
 ; APPLICANT: EDELMAN, Gerald M.  
 ; APPLICANT: CHAPPELL, Stephen A.  
 ; APPLICANT: JONES, Frederick S.  
 ; APPLICANT: OWENS, Geoffrey  
 ; APPLICANT: MEECH, Robin  
 ; TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATIONAL  
 ; TITLE OF INVENTION: REGULATORY ELEMENTS, AND COMPOSITIONS RELATING TO SAME  
 ; FILE REFERENCE: SCRIPI380-1  
 ; CURRENT APPLICATION NUMBER: US/10/182,329  
 ; CURRENT FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: PCT/US 01/02733  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: US 60/261,312  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: US 60/230,956  
 ; PRIOR FILING DATE: 2000-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/230,852  
 ; PRIOR FILING DATE: 2000-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/207,804  
 ; PRIOR FILING DATE: 2000-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/186,496  
 ; PRIOR FILING DATE: 2000-03-02  
 ; PRIOR APPLICATION NUMBER: US 60/178,816  
 ; NUMBER OF SEQ ID NOS: 112  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 109  
 ; LENGTH: 6250  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: VECTOR  
 US-10-182-329-109

Query Match 33.5%; Score 175.2; DB 15; Length 6250;  
 Best Local Similarity 98.3%; Pred. No. 3e-49;  
 Matches 177; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 259 AAATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGATTAGCAAC 318  
 DB 3164 AAATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGATTAGCAAC 3223  
 QY 319 ATGCTTACAGGAGAGAAAAAGCAACCGTGCATGCCGATTGGTGAAGTAAGGTGGTAGC 378  
 DB 3224 ATGCTTACAGGAGAGAAAAAGCAACCGTGCATGCCGATTGGTGAAGTAAGGTGGTAGC 3283  
 QY 379 ATGCTGCTTATTAGGAAGGCAACGAGCGGTCTGACATGGATTGGACGAACCACTAAAT 438  
 DB 3284 ATGCTGCTTATTAGGAAGGCAACGAGCGGTCTGACATGGATTGGACGAACCACTAGAT 3343

## RESULT 29

US-10-182-329-1  
 ; Sequence 1, Application US/10182329  
 ; Publication No. US20040005564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
 ; APPLICANT: MAURO, Vincent P.





; OTHER INFORMATION: 1

; APPLICANT: Livingston, Br

; OTHER INFORMATION: i

```

; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 5053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pep2
US-10-371-069-35

Query Match      28.9%; Score 151.4; DB 15; Length 5053;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGGTTAGCGGTTTGG 120
DB 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGGTTAGCGGTTTGG 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

```

```

RESULT 35
US-10-371-645-35
; Sequence 35, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 5053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pep2
US-10-371-645-35

Query Match      28.9%; Score 151.4; DB 15; Length 5053;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGGTTAGCGGTTTGG 120
DB 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGGTTAGCGGTTTGG 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

```

```

RESULT 36
US-10-371-260-35
; Sequence 35, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 5053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pep2
US-10-371-260-35

Query Match      28.9%; Score 151.4; DB 15; Length 5053;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGGTTAGCGGTTTGG 120
DB 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGGTTAGCGGTTTGG 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

```

```

RESULT 37
US-09-795-006A-41
; Sequence 41, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalia et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26

```

QY 61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 120

```

Db      141 ACAAGCAAGGCTTACCGGCAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 200
QY      121 CTGCTTCGGGATGTACGGGCGAGATATTCGGGT 153
Db      201 CTGCTTCGGGATGTACGGGCGAGATATTCGGGT 233

RESULT 41
US-10-161-403-26
; Sequence 26, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 5162
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric bacterial plasmid
US-10-161-403-26

```

```

Query Match      28.9%; Score 151.4; DB 14; Length 5162;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTTGGAGTTCCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db      81 CTGCTCCCTGCTGTGTGTTGGAGTTCCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140
QY      61 ACAAGCAAGGCTTACCGGCAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 120
Db      141 ACAAGCAAGGCTTACCGGCAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 200
QY      121 CTGCTTCGGGATGTACGGGCGAGATATTCGGGT 153
Db      201 CTGCTTCGGGATGTACGGGCGAGATATTCGGGT 233

```

```

RESULT 42
US-10-086-745-13
; Sequence 13, Application US/10086745
; Publication No. US20030186390A1
; GENERAL INFORMATION:
; APPLICANT: de Jong, Gary
; APPLICANT: Vandebyl, Sandra
; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID
; FILE REFERENCE: 24601-416C
; CURRENT APPLICATION NUMBER: US/10/086,745
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5162
; TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric bacterial plasmid
US-10-086-745-13

Query Match      28.9%; Score 151.4; DB 14; Length 5162;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTTGGAGTTCCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db      81 CTGCTCCCTGCTGTGTGTTGGAGTTCCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140
QY      61 ACAAGCAAGGCTTACCGGCAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 120
Db      141 ACAAGCAAGGCTTACCGGCAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 200
QY      121 CTGCTTCGGGATGTACGGGCGAGATATTCGGGT 153
Db      201 CTGCTTCGGGATGTACGGGCGAGATATTCGGGT 233

```

```

RESULT 43
US-10-005-876A-73
; Sequence 73, Application US/10005876A
; Publication No. US20030186233A1
; GENERAL INFORMATION:
; APPLICANT: Chesnut, Jonathan D.
; APPLICANT: Carrino, John
; APPLICANT: Leong, Louis
; APPLICANT: Madden, Knut
; APPLICANT: Gleeson, Martin
; APPLICANT: Fan, James
; APPLICANT: Brasch, Michael A.
; APPLICANT: Cheo, David
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; APPLICANT: Temple, Gary F.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Nucleic Acid
; FILE REFERENCE: 0942,5340002
; CURRENT APPLICATION NUMBER: US/10/005,876A
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/254,510
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,972
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/318,902
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/326,092
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/333,124
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 09/732,914
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 5173
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of plasmid pCDNA6.2/V5/GWD-TOPO
; NAME/KEY: unsure
; LOCATION: (958)..(966)
; OTHER INFORMATION: "n" can be any nucleotide: a, t, c, g
US-10-005-876A-73

```

```

Query Match      28.9%; Score 151.4; DB 14; Length 5173;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTGGC 120  
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTGGC 200  
QY 121 CTGCTCCGATGATGACGGCCAGATATTCGCGT 153  
Db 201 CTGCTCCGATGATGACGGCCAGATATTCGCGT 233

## RESULT 44

US-10-161-403-88  
; Sequence 88, Application US/10161403  
; Publication No. US20030119104A1  
; GENERAL INFORMATION:  
; APPLICANT: Perkins, Edward  
; APPLICANT: Perez, Carl  
; APPLICANT: Lindenbaum, Michael  
; APPLICANT: Greene, Amy  
; APPLICANT: Leung, Josephine  
; APPLICANT: Fleming, Elena  
; APPLICANT: Stewart, Sandra  
; APPLICANT: Shellard, Joan  
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS  
; FILE REFERENCE: 24601-420  
; CURRENT APPLICATION NUMBER: US/10/161,403  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/294,758  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/366,891  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88  
; LENGTH: 5192  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pIRSpuro2 plasmid from Clontech  
US-10-161-403-88

Query Match 28.9%; Score 151.4; DB 14; Length 5192;  
Best Local Similarity 99.3%; Pred. No. 4.7e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTGGC 120  
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTGGC 200  
QY 121 CTGCTCCGATGATGACGGCCAGATATTCGCGT 153  
Db 201 CTGCTCCGATGATGACGGCCAGATATTCGCGT 233

## RESULT 45

US-09-826-115-23  
; Sequence 23, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.033203  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298

; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 5271  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; NAME/KEY: CDS  
; LOCATION: (910)...(2953)  
US-09-826-115-23

Query Match 28.9%; Score 151.4; DB 10; Length 5271;  
Best Local Similarity 99.3%; Pred. No. 4.8e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTGGC 120  
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGCTTAGGCGTTTGGC 200  
QY 121 CTGCTCCGATGATGACGGCCAGATATTCGCGT 153  
Db 201 CTGCTCCGATGATGACGGCCAGATATTCGCGT 233

## RESULT 46

US-09-826-115-19  
; Sequence 19, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.033203  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 5283  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; NAME/KEY: CDS  
; LOCATION: (910)...(2965)  
US-09-826-115-19

Query Match 28.9%; Score 151.4; DB 10; Length 5283;  
Best Local Similarity 99.3%; Pred. No. 4.8e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

```
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 120
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 200
QY 121 CTGCTCCGCGATGACGGCCAGATATTCGGT 153
Db 201 CTGCTCCGCGATGACGGCCAGATATTCGGT 233
```

## RESULT 47

```
US-09-826-115-21
; Sequence 21, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
; FILE REFERENCE: 14114.0332U3
; CURRENT APPLICATION NUMBER: US/09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: pct/us99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; NAME/KEY: CDS
; LOCATION: (910)...(2986)
US-09-826-115-21
```

```
Query Match 28.9%; Score 151.4; DB 10; Length 5304;
Best Local Similarity 99.3%; Pred. No. 4.8e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCGCGATGACGGCCAGATATTCGGT 153
Db 81 CTGCTCCGCGATGACGGCCAGATATTCGGT 233
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 120
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 200
QY 121 CTGCTCCGCGATGACGGCCAGATATTCGGT 153
Db 201 CTGCTCCGCGATGACGGCCAGATATTCGGT 233
```

## RESULT 48

```
US-09-826-115-15
; Sequence 15, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
; FILE REFERENCE: 14114.0332U3
; CURRENT APPLICATION NUMBER: US/09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: pct/us99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
```

```
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 5308
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
; NAME/KEY: CDS
; LOCATION: (911)...(2987)
; NAME/KEY: misc Feature
; LOCATION: (1)...(5308)
; OTHER INFORMATION: pCEWJN
US-09-826-115-15
```

```
Query Match 28.9%; Score 151.4; DB 10; Length 5308;
Best Local Similarity 99.3%; Pred. No. 4.8e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCGCGATGACGGCCAGATATTCGGT 153
Db 81 CTGCTCCGCGATGACGGCCAGATATTCGGT 233
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 120
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 200
QY 121 CTGCTCCGCGATGACGGCCAGATATTCGGT 153
Db 201 CTGCTCCGCGATGACGGCCAGATATTCGGT 233
```

## RESULT 49

```
US-09-826-115-17
; Sequence 17, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
; FILE REFERENCE: 14114.0332U3
; CURRENT APPLICATION NUMBER: US/09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: pct/us99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 5334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
; NAME/KEY: CDS
; LOCATION: (916)...(3007)
; NAME/KEY: misc Feature
; LOCATION: (1)...(5334)
; OTHER INFORMATION: pCEJE 1-14
US-09-826-115-17
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Query Match 28.9%; Score 151.4; DB 10; Length 5334;
Best Local Similarity 99.3%; Pred. No. 4.8e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCGCGATGACGGCCAGATATTCGGT 153
Db 81 CTGCTCCGCGATGACGGCCAGATATTCGGT 233
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QY 61 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 200  
 Db |||||  
 QY 121 CTGCTCCGCGATGTACGGGCGAGATATTCGGGT 153  
 Db |||||  
 QY 201 CTGCTCCGCGATGTACGGGCGAGATATTCGGGT 233  
 Db |||||

# RESULT 50

US-09-794-975-9  
 ; Sequence 9, Application US/09794975  
 ; Patent No. US20010034884A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PERAUS, Gisela  
 ; TITLE OF INVENTION: A-BETA PEPTIDE SCREENING ASSAY  
 ; FILE REFERENCE: 514429-3785  
 ; CURRENT APPLICATION NUMBER: US/09/794,975  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: US 09/455,367  
 ; PRIOR FILING DATE: 1999-12-03  
 ; PRIOR APPLICATION NUMBER: 19856261.6  
 ; PRIOR FILING DATE: 1998-12-07  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 5432  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: mutagen  
 US-09-794-975-9

Query Match 28.9%; Score 151.4; DB 9; Length 5432;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTTGGAGTCCCTAGTGTGCGGCAAAATTTAAGCTACA 60  
 Db |||||  
 QY 81 CTGCTCCCTGCTTGTGTTGGAGTCCCTAGTGTGCGGCAAAATTTAAGCTACA 140  
 Db |||||  
 QY 61 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 200  
 Db |||||  
 QY 121 CTGCTCCGCGATGTACGGGCGAGATATTCGGGT 153  
 Db |||||  
 QY 201 CTGCTCCGCGATGTACGGGCGAGATATTCGGGT 233  
 Db |||||

# RESULT 51

US-09-844-645-3  
 ; Sequence 3, Application US/09844645  
 ; Patent No. US2002010242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Briles, David E.  
 ; McDaniel, Larry S.  
 ; Curitel, David T.  
 ; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
 ; ADMINISTERING PNEUMOCOCCAL DNA  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Curitel, Morris & Safford, P.C.  
 ; STREET: 530 Fifth Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/844,645  
 ; FILING DATE: 27-Apr-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/759,505  
 ; FILING DATE: 04-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Frommer, William S.  
 ; REGISTRATION NUMBER: 25,506  
 ; REFERENCE/DOCKET NUMBER: 454312-2450  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 840-3333  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5446 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-844-645-3

Query Match 28.9%; Score 151.4; DB 9; Length 5446;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTTGGAGTCCCTAGTGTGCGGCAAAATTTAAGCTACA 60  
 Db |||||  
 QY 81 CTGCTCCCTGCTTGTGTTGGAGTCCCTAGTGTGCGGCAAAATTTAAGCTACA 140  
 Db |||||  
 QY 61 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 200  
 Db |||||  
 QY 121 CTGCTCCGCGATGTACGGGCGAGATATTCGGGT 153  
 Db |||||  
 QY 201 CTGCTCCGCGATGTACGGGCGAGATATTCGGGT 233  
 Db |||||

# RESULT 52

US-09-559-874-5  
 ; Sequence 5, Application US/09559874  
 ; Publication No. US20020192726A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leng, Jay  
 ; TITLE OF INVENTION: CELL PROLIFERATION ASSAY  
 ; FILE REFERENCE: 105175-159906  
 ; CURRENT APPLICATION NUMBER: US/09/559,874  
 ; CURRENT FILING DATE: 2000-04-25  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 5446  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: pcDNA3 vector  
 ; OTHER INFORMATION: sequence  
 US-09-559-874-5

Query Match 28.9%; Score 151.4; DB 9; Length 5446;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTTGGAGTCCCTAGTGTGCGGCAAAATTTAAGCTACA 60  
 Db |||||  
 QY 81 CTGCTCCCTGCTTGTGTTGGAGTCCCTAGTGTGCGGCAAAATTTAAGCTACA 140  
 Db |||||  
 QY 61 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGGCTTACCGACAAATTCATGAAGAATCTGCTTAGGCTAGCGGTTTGGG 200  
 Db |||||

QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233  
 RESULT 53  
 US-10-371-116A-1  
 ; Sequence 11, Application US/10371116A  
 ; Publication No. US20040005588A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.  
 ; TITLE OF INVENTION: METHODS OF TREATMENT OR PREVENTION OF AUTOIMMUNE DISEASES  
 ; FILE REFERENCE: 87534-3900  
 ; CURRENT APPLICATION NUMBER: US/10/371,116A  
 ; PRIOR FILING DATE: 2003-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/227, 853  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 5446  
 ; TYPE: DNA  
 ; ORGANISM: artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: pcDNA3 vector nucleotide sequence  
 US-10-371-116A-1  
 Query Match 28.9%; Score 151.4; DB 15; Length 5446;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 200  
 QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233  
 RESULT 54  
 US-09-912-436-11  
 ; Sequence 11, Application US/09912436  
 ; Patent No. US20020068694A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JEITSCH, Markku M  
 ; APPLICANT: ALITALO, Kari  
 ; APPLICANT: OLOFSSON, Birgitta  
 ; APPLICANT: ERIKSSON, Ulf  
 ; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
 ; FILE REFERENCE: 1064-48929PV Markku JEITSCH et al  
 ; CURRENT APPLICATION NUMBER: US/09/912,436  
 ; PRIOR FILING DATE: 2001-07-26  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 5458  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: pSectaga-VEGF-BEX1-5-H6  
 US-09-912-436-11  
 Query Match 28.9%; Score 151.4; DB 9; Length 5458;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 200  
 QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233  
 RESULT 55  
 US-09-912-436-12  
 ; Sequence 12, Application US/09912436  
 ; Patent No. US20020068694A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JEITSCH, Markku M  
 ; APPLICANT: ALITALO, Kari  
 ; APPLICANT: OLOFSSON, Birgitta  
 ; APPLICANT: ERIKSSON, Ulf  
 ; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
 ; FILE REFERENCE: 1064-48929PV Markku JEITSCH et al  
 ; CURRENT APPLICATION NUMBER: US/09/912,436  
 ; PRIOR FILING DATE: 2001-07-26  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 12  
 ; LENGTH: 5458  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: pSectaga-VEGF-BEX1-5-H6-NKT  
 US-09-912-436-12  
 Query Match 28.9%; Score 151.4; DB 9; Length 5458;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 200  
 QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233  
 RESULT 56  
 US-10-005-876A-72  
 ; Sequence 72, Application US/10005876A  
 ; Publication No. US20030186233A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chesnut, Jonathan D.  
 ; APPLICANT: Carrino, John  
 ; APPLICANT: Leong, Louis  
 ; APPLICANT: Madden, Knut  
 ; APPLICANT: Gleeson, Martin  
 ; APPLICANT: Fan, James  
 ; APPLICANT: Brasch, Michael A.  
 ; APPLICANT: Cheo, David  
 ; APPLICANT: Hartley, James L.  
 ; APPLICANT: Byrd, Devon R.N.  
 ; APPLICANT: Temple, Gary F.  
 US-10-005-876A-72  
 Query Match 28.9%; Score 151.4; DB 9; Length 5458;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 200  
 QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233

Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 200  
 QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233  
 RESULT 55  
 US-09-912-436-12  
 ; Sequence 12, Application US/09912436  
 ; Patent No. US20020068694A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JEITSCH, Markku M  
 ; APPLICANT: ALITALO, Kari  
 ; APPLICANT: OLOFSSON, Birgitta  
 ; APPLICANT: ERIKSSON, Ulf  
 ; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
 ; FILE REFERENCE: 1064-48929PV Markku JEITSCH et al  
 ; CURRENT APPLICATION NUMBER: US/09/912,436  
 ; PRIOR FILING DATE: 2001-07-26  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 12  
 ; LENGTH: 5458  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: pSectaga-VEGF-BEX1-5-H6-NKT  
 US-09-912-436-12  
 Query Match 28.9%; Score 151.4; DB 9; Length 5458;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 200  
 QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233  
 RESULT 56  
 US-10-005-876A-72  
 ; Sequence 72, Application US/10005876A  
 ; Publication No. US20030186233A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chesnut, Jonathan D.  
 ; APPLICANT: Carrino, John  
 ; APPLICANT: Leong, Louis  
 ; APPLICANT: Madden, Knut  
 ; APPLICANT: Gleeson, Martin  
 ; APPLICANT: Fan, James  
 ; APPLICANT: Brasch, Michael A.  
 ; APPLICANT: Cheo, David  
 ; APPLICANT: Hartley, James L.  
 ; APPLICANT: Byrd, Devon R.N.  
 ; APPLICANT: Temple, Gary F.  
 US-10-005-876A-72  
 Query Match 28.9%; Score 151.4; DB 9; Length 5458;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 120  
 Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGCGGTTTGGC 200  
 QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233



;; TITLE OF INVENTION: Methods and Compositions for Synthesis of Nucleic Acid  
;; FILE REFERENCE: 0942.5340002  
;; CURRENT APPLICATION NUMBER: US/10/005,876A  
;; PRIOR FILING DATE: 2001-12-03  
;; PRIOR APPLICATION NUMBER: 60/254,510  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/291,972  
;; PRIOR FILING DATE: 2001-05-21  
;; PRIOR APPLICATION NUMBER: 60/318,902  
;; PRIOR FILING DATE: 2001-09-14  
;; PRIOR APPLICATION NUMBER: 60/326,092  
;; PRIOR FILING DATE: 2001-09-28  
;; PRIOR APPLICATION NUMBER: 60/333,124  
;; PRIOR FILING DATE: 2001-11-27  
;; PRIOR APPLICATION NUMBER: 09/732,914  
;; PRIOR FILING DATE: 2000-12-11  
;; NUMBER OF SEQ ID NOS: 80  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 72  
;; LENGTH: 5543  
;; TYPE: DNA  
;; ORGANISM: artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Nucleotide sequence of plasmid pCDNA3.2/V5/GW-D-TOPO  
;; NAME/KEY: unsure  
;; LOCATION: (958)..(966)  
;; OTHER INFORMATION: "n" can be any nucleotide: a, t, c, g  
US-10-005-876A-72

Query Match 28.9%; Score 151.4; DB 14; Length 5543;  
Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 200  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 57  
US-09-912-436-7  
; Sequence 7; Application US/09912436  
; Patent No. US2002008694A1  
; GENERAL INFORMATION:  
; APPLICANT: JELTSCH, Markku M  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ERIKSSON, Ulf  
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
; FILE REFERENCE: AMOUNT OF SOLUBLE VEGF-B  
; CURRENT APPLICATION NUMBER: US/09/912,436  
; CURRENT FILING DATE: 2001-07-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 5614  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: pSectAgA-VEGF-B167-H6  
US-09-912-436-7

Query Match 28.9%; Score 151.4; DB 9; Length 5614;  
Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 200  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 58  
US-09-912-436-8  
; Sequence 8; Application US/09912436  
; Patent No. US2002008694A1  
; GENERAL INFORMATION:  
; APPLICANT: JELTSCH, Markku M  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ERIKSSON, Ulf  
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
; FILE REFERENCE: AMOUNT OF SOLUBLE VEGF-B  
; CURRENT APPLICATION NUMBER: US/09/912,436  
; CURRENT FILING DATE: 2001-07-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 5614  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: pSectAgA-VEGF-B167-H6-NXT  
US-09-912-436-8

Query Match 28.9%; Score 151.4; DB 9; Length 5614;  
Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 200  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 59  
US-10-142-358-1  
; Sequence 1; Application US/10142358  
; Publication No. US20030083291A1  
; GENERAL INFORMATION:  
; APPLICANT: Michel, Marie-Louise  
; APPLICANT: Mancine, Maryline  
; TITLE OF INVENTION: Nucleotide Vector, Composition  
; Containing Such Vector, and Vaccine for Immunization  
; Against Hepatitis  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; Turner

```
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/142,358
; FILING DATE: 10-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,569
; FILING DATE: 12-FEB-1997
; APPLICATION NUMBER: US 08/706,337
; FILING DATE: 30-AUG-1996
; APPLICATION NUMBER: US 08/633,821
; FILING DATE: 22-APR-1996
; APPLICATION NUMBER: FR 94/00483
; FILING DATE: 27-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0128-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-142-358-1

Query Match      28.9%; Score 151.4; DB 14; Length 5618;
Best Local Similarity 99.3%; Pred. No. 4.9e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTAAGCTACA 60
Db      81 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTAAGCTACA 140
QY      61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGCTTAGCGTTTGG 120
Db      141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGCTTAGCGTTTGG 200
QY      121 CTGCTTCGGATGACGGGCCAGATATTCGGT 153
Db      201 CTGCTTCGGATGACGGGCCAGATATTCGGT 233

RESULT 60
US-09-780-933-6
; Sequence 6, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHMAYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
```

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; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1231)..(1617)
US-09-780-933-6

Query Match      28.9%; Score 151.4; DB 9; Length 5651;
Best Local Similarity 99.3%; Pred. No. 5e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTAAGCTACA 60
Db      81 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTAAGCTACA 140
QY      61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGCTTAGCGTTTGG 120
Db      141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGCTTAGCGTTTGG 200
QY      121 CTGCTTCGGATGACGGGCCAGATATTCGGT 153
Db      201 CTGCTTCGGATGACGGGCCAGATATTCGGT 233

RESULT 61
US-09-896-896A-4
; Sequence 4, Application US/09896896A
; Publication No. US20030036181A1
; GENERAL INFORMATION:
; APPLICANT: MAXYGEN APS
; TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
; FILE REFERENCE: 0217us210
; CURRENT APPLICATION NUMBER: US/09/896,896A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/225,558
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: DK PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: PCT/DK00/00743
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/DK01/00090
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5651
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1231)..(1617)
; OTHER INFORMATION: Coding sequence for human FSH-beta
US-09-896-896A-4

Query Match      28.9%; Score 151.4; DB 10; Length 5651;
Best Local Similarity 99.3%; Pred. No. 5e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTAAGCTACA 60
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Db      81 CTGCTCCCTGCTTGTGTGTGGAGTCTGCTGAGTAGTGGCGGACGCAAAATTTAGCTACA 140
QY      61 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 120
Db      141 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 200
QY      121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153
Db      201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

```

## RESULT 62

```

US-09-912-436-9
; Sequence 9, Application US/09912436
; Patent No. US20020068694A1
; GENERAL INFORMATION:
; APPLICANT: JELTSCH, Markku M
; APPLICANT: ALITALO, Kari
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ERIKSSON, Ulf
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE
; FILE REFERENCE: 1064-48923PV Markku JELTSCH et al
; CURRENT APPLICATION NUMBER: US/09/912,436
; CURRENT FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5695
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pSectaga-VEGF-B186-H6-NYT
US-09-912-436-9

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```

Query Match      28.9%; Score 151.4; DB 9; Length 5695;
Best Local Similarity 99.3%; Pred. No. 5e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTTGTGTGTGGAGTCTGCTGAGTAGTGGCGGACGCAAAATTTAGCTACA 60
Db      81 CTGCTCCCTGCTTGTGTGTGGAGTCTGCTGAGTAGTGGCGGACGCAAAATTTAGCTACA 140
QY      61 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 120
Db      141 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 200
QY      121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153
Db      201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

```

## RESULT 63

```

US-09-912-436-10
; Sequence 10, Application US/09912436
; Patent No. US20020068694A1
; GENERAL INFORMATION:
; APPLICANT: JELTSCH, Markku M
; APPLICANT: ALITALO, Kari
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ERIKSSON, Ulf
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE
; FILE REFERENCE: 1064-48923PV Markku JELTSCH et al
; CURRENT APPLICATION NUMBER: US/09/912,436
; CURRENT FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5695
; TYPE: DNA

```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pSectaga-VEGF-B186-H6
US-09-912-436-10

```

```

Query Match      28.9%; Score 151.4; DB 9; Length 5695;
Best Local Similarity 99.3%; Pred. No. 5e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTTGTGTGTGGAGTCTGCTGAGTAGTGGCGGACGCAAAATTTAGCTACA 60
Db      81 CTGCTCCCTGCTTGTGTGTGGAGTCTGCTGAGTAGTGGCGGACGCAAAATTTAGCTACA 140
QY      61 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 120
Db      141 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 200
QY      121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153
Db      201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

```

## RESULT 64

```

US-09-765-555-66
; Sequence 66, Application US/09765555
; Publication No. US20030037355A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to modulate
; FILE REFERENCE: 27801-20014.40
; CURRENT APPLICATION NUMBER: US/09/765,555
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/620,897
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 5731
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2C7-SID
US-09-765-555-66

```

```

Query Match      28.9%; Score 151.4; DB 10; Length 5731;
Best Local Similarity 99.3%; Pred. No. 5e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTTGTGTGTGGAGTCTGCTGAGTAGTGGCGGACGCAAAATTTAGCTACA 60
Db      81 CTGCTCCCTGCTTGTGTGTGGAGTCTGCTGAGTAGTGGCGGACGCAAAATTTAGCTACA 140
QY      61 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 120
Db      141 ACAAGGCAAGGCTTGCACGCAATTCATGATGAAGATCTGCTTAGGCTTAGGCTTTTGG 200
QY      121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153
Db      201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

```

## RESULT 65

```

US-09-971-980-1
; Sequence 1, Application US/09971980
; Patent No. US20020164349A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses

```

;; TITLE OF INVENTION: Pestiviruses  
;; FILE REFERENCE: Upn-4105  
;; CURRENT APPLICATION NUMBER: US/09/971,980  
;; PRIOR FILING DATE: 2001-10-04  
;; PRIOR APPLICATION NUMBER: 60/237,885  
;; PRIOR FILING DATE: 2000-10-04  
;; NUMBER OF SEQ ID NOS: 73  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1  
;; LENGTH: 5864  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Plasmid  
US-09-971-980-1

Query Match 28.9%; Score 151.4; DB 9; Length 5864;  
Best Local Similarity 99.3%; Pred. No. 5.1e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGACAATTCATGAGATCTGCTTAGGTTAGCGGTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCATGAGATCTGCTTAGGTTAGCGGTTTGG 200

Qy 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 153  
Db 201 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 233

RESULT 66  
US-09-971-980-4  
;; Sequence 4, Application US/09971980  
;; Patent No. US20020164349A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Weinez, David B.  
;; APPLICANT: Yang, Joo-Sung  
;; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flavivirus  
;; FILE REFERENCE: Upn-4105  
;; CURRENT APPLICATION NUMBER: US/09/971,980  
;; CURRENT FILING DATE: 2001-10-04  
;; PRIOR APPLICATION NUMBER: 60/237,885  
;; PRIOR FILING DATE: 2000-10-04  
;; NUMBER OF SEQ ID NOS: 73  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 4  
;; LENGTH: 5864  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Plasmid  
US-09-971-980-4

Query Match 28.9%; Score 151.4; DB 9; Length 5864;  
Best Local Similarity 99.3%; Pred. No. 5.1e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGACAATTCATGAGATCTGCTTAGGTTAGCGGTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCATGAGATCTGCTTAGGTTAGCGGTTTGG 200

Qy 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 153  
Db 201 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 233

RESULT 67  
US-10-395-894-8  
;; Sequence 8, Application US/10395894  
;; Publication No. US20040033229A1  
;; GENERAL INFORMATION:  
;; APPLICANT: MADDON, Paul J.  
;; APPLICANT: DONOVAN, Gerald P.  
;; APPLICANT: OLSON, William C.  
;; APPLICANT: SCHLKE, No. US20040033229A1  
;; APPLICANT: GARDNER, Jason  
;; APPLICANT: MA, Dangshe  
;; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
;; FILE REFERENCE: P00741.70005.US  
;; CURRENT APPLICATION NUMBER: US/10/395,894  
;; CURRENT FILING DATE: 2003-03-24  
;; PRIOR APPLICATION NUMBER: PCI/US02/33944  
;; PRIOR FILING DATE: 2002-10-23  
;; PRIOR APPLICATION NUMBER: US 60/335,215  
;; PRIOR FILING DATE: 2001-10-23  
;; PRIOR APPLICATION NUMBER: US 60/362,747  
;; PRIOR APPLICATION NUMBER: US 60/412,618  
;; PRIOR FILING DATE: 2002-09-20  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 8  
;; LENGTH: 6082  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Plasmid  
US-10-395-894-8

Query Match 28.9%; Score 151.4; DB 12; Length 6082;  
Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGACAATTCATGAGATCTGCTTAGGTTAGCGGTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCATGAGATCTGCTTAGGTTAGCGGTTTGG 200

Qy 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 153  
Db 201 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 233

RESULT 68  
US-10-395-894-9  
;; Sequence 9, Application US/10395894  
;; Publication No. US20040033229A1  
;; GENERAL INFORMATION:  
;; APPLICANT: MADDON, Paul J.  
;; APPLICANT: DONOVAN, Gerald P.  
;; APPLICANT: OLSON, William C.  
;; APPLICANT: SCHLKE, No. US20040033229A1  
;; APPLICANT: GARDNER, Jason  
;; APPLICANT: MA, Dangshe  
;; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
;; FILE REFERENCE: P00741.70005.US  
;; CURRENT APPLICATION NUMBER: US/10/395,894  
;; CURRENT FILING DATE: 2003-03-24  
;; PRIOR APPLICATION NUMBER: PCI/US02/33944  
;; PRIOR FILING DATE: 2002-10-23  
;; PRIOR APPLICATION NUMBER: US 60/335,215  
;; PRIOR FILING DATE: 2001-10-23  
;; PRIOR APPLICATION NUMBER: US 60/362,747  
;; PRIOR FILING DATE: 2002-03-07  
;; PRIOR APPLICATION NUMBER: US 60/412,618

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/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 9
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-9

Query Match      28.9%; Score 151.4; DB 12; Length 6082;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200

QY 121 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 153
DB 201 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 233

RESULT 69
US-10-395-894-10
/ Sequence 10, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHSLKE, No. US20040033229Albert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/335,215
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: US 60/362,747
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/412,618
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 10
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-10

Query Match      28.9%; Score 151.4; DB 12; Length 6082;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200

QY 121 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 153
DB 201 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 233

RESULT 69
US-10-395-894-10
/ Sequence 10, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHSLKE, No. US20040033229Albert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/335,215
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: US 60/362,747
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/412,618
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 10
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-10

Query Match      28.9%; Score 151.4; DB 12; Length 6082;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200
```

```
QY 121 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 153
DB 201 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 233

RESULT 70
US-10-395-894-11
/ Sequence 11, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHSLKE, No. US20040033229Albert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/335,215
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: US 60/362,747
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/412,618
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 11
/ LENGTH: 6085
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-11

Query Match      28.9%; Score 151.4; DB 12; Length 6085;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200

QY 121 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 153
DB 201 CTGCTTCGGGATGACGGGCCAGATATTCGGGT 233

RESULT 71
US-10-395-894-13
/ Sequence 13, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHSLKE, No. US20040033229Albert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/335,215
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 13
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-13

Query Match      28.9%; Score 151.4; DB 12; Length 6082;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200
```

; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 6094  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid  
US-10-395-894-13

Query Match 28.9%; Score 151.4; DB 12; Length 6094;  
Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 81 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGCTTGACCGACAAATTCATGAAGATCTGCTTAGGGTTAGGGGTTTTCGG 120  
DB 141 ACAAGGCAAGCTTGACCGACAAATTCATGAAGATCTGCTTAGGGTTAGGGGTTTTCGG 200  
QY 121 CTGCTTCCGATGTACGGCCAGATATTTCGGCT 153  
DB 201 CTGCTTCCGATGTACGGCCAGATATTTCGGCT 233

RESULT 72  
US-10-395-894-12  
; Sequence 12, Application US/10395894  
; Publication No. US20040033229A1  
; GENERAL INFORMATION:  
; APPLICANT: MADON, Paul J.  
; APPLICANT: DONOVAN, Gerald P.  
; APPLICANT: OLSON, William C.  
; APPLICANT: SCHLKE, No. US20040033229A1bert  
; APPLICANT: GARDNER, Jason  
; APPLICANT: MA, Dangehe  
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
; FILE REFERENCE: P00741.70005.US  
; CURRENT APPLICATION NUMBER: US/10/395,894  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/335,215  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 6097  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid  
US-10-395-894-12

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Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
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QY 61 ACAAGGCAAGCTTGACCGACAAATTCATGAAGATCTGCTTAGGGTTAGGGGTTTTCGG 120  
DB 141 ACAAGGCAAGCTTGACCGACAAATTCATGAAGATCTGCTTAGGGTTAGGGGTTTTCGG 200  
QY 121 CTGCTTCCGATGTACGGCCAGATATTTCGGCT 153  
DB 201 CTGCTTCCGATGTACGGCCAGATATTTCGGCT 233

RESULT 73  
US-09-884-211A-5  
; Sequence 5, Application US/09884211A  
; Publication No. US20030032791A1  
; GENERAL INFORMATION:  
; APPLICANT: Alan et. al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: P010743A  
; CURRENT APPLICATION NUMBER: US/09/884,211A  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 6148  
; TYPE: DNA  
; ORGANISM: pcDNA3.1zeo/murine G-alpha 15  
US-09-884-211A-5

Query Match 28.9%; Score 151.4; DB 10; Length 6148;  
Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
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QY 1 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
DB 81 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGCTTGACCGACAAATTCATGAAGATCTGCTTAGGGTTAGGGGTTTTCGG 120  
DB 141 ACAAGGCAAGCTTGACCGACAAATTCATGAAGATCTGCTTAGGGTTAGGGGTTTTCGG 200  
QY 121 CTGCTTCCGATGTACGGCCAGATATTTCGGCT 153  
DB 201 CTGCTTCCGATGTACGGCCAGATATTTCGGCT 233

RESULT 74  
US-09-884-211A-6  
; Sequence 6, Application US/09884211A  
; Publication No. US20030032791A1  
; GENERAL INFORMATION:  
; APPLICANT: Alan et. al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: P010743A  
; CURRENT APPLICATION NUMBER: US/09/884,211A  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 6149  
; TYPE: DNA  
; ORGANISM: pcDNA3.1zeo/human G-alpha 16  
US-09-884-211A-6

Query Match 28.9%; Score 151.4; DB 10; Length 6149;  
Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: March 11, 2004, 11:20:19  
Job time : 386.636 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 07:44:02 ; Search time 3117.7 seconds  
(without alignments)  
5009.444 Million cell updates/sec

Title: US-09-733-368a-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgcctccctgtgtgtgtt.....accacattggtgcaccc 523

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estim.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfum.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pin.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vri.\*  
28: gb\_gsal.\*  
29: gb\_gsa2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	196.8	37.6	865	14	CF251529 hdm001_c0
3	151	28.9	863	14	CF251728 hdm003_e1
4	103.8	13.8	377	12	B1065864 pgfln.pko

5	103.8	19.8	414	14	CF250631
6	103.8	19.8	454	14	CF250926
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8	103.8	19.8	661	13	BUI338428
9	103.8	19.8	668	13	BUI452326
10	103.8	19.8	673	13	BUI04175
11	103.8	19.8	728	13	BUI17201
12	103.8	19.8	741	13	BUI25810
13	103.8	19.8	777	13	BUI470589
14	103.8	19.8	784	13	BUI444255
15	103.8	19.8	793	13	BUI312414
16	103.8	19.8	801	13	BUI07637
17	103.8	19.8	834	13	BUI14728
18	103.8	19.8	835	13	BUI413305
19	103.8	19.8	859	13	BUI354615
20	103	19.7	725	13	BUI490656
21	102.2	19.5	773	13	BUI32452
22	100.6	19.2	732	13	BUI343905
23	100.6	19.2	744	13	BUI309030
24	100.6	19.2	1012	13	BUI43329
25	95	18.2	695	13	BUI490989
26	93.6	17.9	270	14	CB016682
27	93.4	17.9	669	13	BUI263560
28	92.8	17.7	810	13	BUI356927
29	88.2	16.9	623	13	BUI492375
30	88	16.8	418	13	BUI404431
31	88	16.8	598	13	BUI490064
32	88	16.8	773	13	BUI487895
33	87.8	16.8	801	13	BUI474299
34	86.4	16.5	282	13	BUI415406
35	86.4	16.5	766	13	BUI471721
36	86.4	16.5	780	13	BUI243776
37	84.8	16.2	269	13	BUI49048
38	80.2	15.3	863	13	BUI340356
39	76	14.5	516	13	BUI201513
40	74.8	14.3	611	13	BUI491086
41	73.8	14.1	647	13	BUI491487
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44	70.4	13.5	773	13	BUI315394
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47	69.2	13.2	851	13	BUI403961
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49	66.6	12.7	630	13	BUI402803
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51	63.6	12.2	376	13	BUI452625
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59	55.8	10.6	576	13	BUI124247
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62	54.6	10.4	750	13	BUI244389
63	53.2	10.2	747	13	BUI413106
64	51.8	9.9	767	13	BUI414993
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66	46.8	8.9	718	13	BUI490848
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82 43.2 8.3 675 13 BU383902  
83 42.6 8.1 605 12 BU390532  
84 41.8 8.0 625 13 BU265554  
85 41.8 8.0 821 13 BU458548  
86 41.8 8.0 1125 28 CC254909  
87 41.2 7.9 676 13 BU247819  
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90 40.8 7.8 726 13 BU260757  
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94 39.8 7.6 577 29 CE028982  
95 39.8 7.6 1134 28 CC246137  
96 39.2 7.5 708 13 BU334817  
97 39.2 7.5 799 13 BU266652  
98 38.6 7.4 635 13 BU393824  
99 38.2 7.3 1095 28 CC215884  
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# ALIGNMENTS

RESULT 1  
B67169  
LOCUS Cp60047A OpIOWAGDNA2 602 bp DNA linear GSS 12-MAY-2000  
DEFINITION Cryptosporidium parvum genomic, genomic survey sequence.  
ACCESSION B67169  
VERSION B67169.1 GI:2642750  
KEYWORDS GSS  
SOURCE Cryptosporidium parvum  
ORGANISM Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
1 (bases 1 to 602)  
Strong, W.B. and Nelson, R.G.  
Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis  
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)  
20184851  
10717299  
Contact: Nelson, R. G.  
Depts. of Medicine & Pharmaceutical Chemistry  
San Francisco General Hospital-University of California, San Francisco  
Box 0811, San Francisco, CA 94143-0811, USA  
Tel: 415 206 8846  
Fax: 415 206 3353  
Email: malaria@itsa.ucsf.edu  
Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalculated bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.  
Seq primer: T7  
Class: shotgun  
High quality sequence stop: 602.  
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between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center  
(http://sequence-www.stanford.edu/group/techdev/shear.htm)  
. The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small fragments and DNA eluting in the void volume was blunt-ended with T4 DNA Polymerase, treated with alkaline phosphatase to prevent the ligation of multiple fragments, ligated to SrfI I-digested pCR-Script Amp (SK+) vector and transformed into E. coli strain XL10 Gold. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."

## ORIGIN

Query Match 99.0%; Score 517.8; DB 28; Length 602;  
Best Local Similarity 99.6%; Pred. No. 4.3e-151;  
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTCTGTTGTGTTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 41 CTGCTCCCTCTGTTGTGTTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 100  
QY 61 ACAAGGCAAGGCTTACCGACCAATTGCATGAGAGATCTGCTTAGGCTTAGGGCTTTGCG 120  
Db 101 ACAAGGCAAGGCTTACCGACCAATTGCATGAGAGATCTGCTTAGGCTTAGGGCTTTGCG 160  
QY 121 CTGCTCCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 161 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 220  
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Db 341 TAAAGTATAGTATAGCAATCCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 400  
QY 361 TGGAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTAT 420  
Db 401 TGGAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTAT 460  
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAGATATGTTATTTAAGTCTAGCTCGATA 480  
Db 461 TTGAGCAACCACTAAATTCGCAATTCGAGAGATATGTTATTTAAGTCTAGCTCGATA 520  
QY 481 CAATAAAGCCATTTGACCAATTCACCAATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 521  
Db 521 CAATAAAGCCATTTGACCAATTCACCAATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561

RESULT 2  
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LOCUS hdm001\_c06 lps-activated macrophage cell line Gallus gallus cdna, mRNA sequence.  
DEFINITION hdm001\_c06 lps-activated macrophage cell line Gallus gallus cdna, mRNA sequence.  
ACCESSION CF251529  
VERSION CF251529.1 GI:33484784  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
REFERENCE 1 (bases 1 to 865)  
AUTHORS Wittzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J., Chausse, A.M. and Zoorob, R.  
TITLE A collection of chicken ESTs from activated immune cells  
JOURNAL Unpublished (2003)

## COMMENT

Contact: Zoorob R  
UPR 1983  
CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
Tel: 33 1 49 58 35 00  
Fax: 33 1 49 58 33 81  
Email: zoorob@vjf.cnrs.fr.

## FEATURES

## source

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## ORIGIN

Query Match 37.6%; Score 196.8; DB 14; Length 865;  
Best Local Similarity 82.7%; Pred. No. 2.5e-50;  
Matches 243; Conservative 0; Mismatches 37; Indels 14; Gaps 1;

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QY 289 CTTCGCAACATGTAACATGAGTTAGCAATGCGCTTACAGGAGAGAAAACACCGTG 348

Db 84 -----GTAAACATGTAACATGAGTTAGCAATGCGCTTATAGGAGAGAAAGGTACCGTG 132

QY 349 CATGCCGATGCTGGAAGTAAAGTGTAGCATGCTGCTTATTAGGAGGCAACAGCGG 408

Db 133 CATGATGATGCTGGAAGTAAAGTGTAGCATGCTGCTTATTAGGAGGTAACAGCGG 192

QY 409 GTCTGACATGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 468

Db 193 GTCTTACACGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 252

QY 469 CTTAGCTGATGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 522

Db 253 GCTAGCTGATGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 306

## RESULT 3

## CF251728

## LOCUS

DEFINITION hm003\_e10 LPS-activated macrophage cell line Gallus gallus cDNA, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Gallus gallus (chicken)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Zoorob R

## UPR 1983

## CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
Tel: 33 1 49 58 35 00  
Fax: 33 1 49 58 33 81  
Email: zoorob@vjf.cnrs.fr.

## FEATURES

## source

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/organism="Gallus gallus"  
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## ORIGIN

Query Match 28.9%; Score 151; DB 14; Length 863;  
Best Local Similarity 81.0%; Pred. No. 5.9e-36;  
Matches 218; Conservative 0; Mismatches 35; Indels 16; Gaps 3;

QY 229 TAGTATGCTTTTCATAGAGGGGAAATAGTCTTATGCAATATCTTCTAGT 288

Db 611 TATGAATAGCTTTTCATAGAGGGGAAATAGTCTTATGCAATATCTTCTAGT 667

QY 289 CTTCGCAACATGTAACATGAGTTAGCAATGCGCTTACAGGAGAGAAAACACCGTG 348

Db 668 -----GTAAACATGTAACATGAGTTAGCAATGCGCTTATAGGAGAG-AGGSGTACCGTG 715

QY 349 CATGCCGATGCTGGAAGTAAAGTGTAGCATGCTGCTTATTAGGAGGCAACAGCGG 408

Db 716 CATGATGATGCTGGAAGTAAAGTGTAGCATGCTGCTTATTAGGAGGTAACAGCGG 775

QY 409 GTCTGACATGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 468

Db 776 GTCTTACACGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 834

QY 469 CTTAGCTGATGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 497

Db 835 GCTAGCTGATGATGGAACCAACCACTAAATTCGCGATTCGAGATATTTGATTTAAGTG 863

## RESULT 4

## BI065864

## LOCUS

## DEFINITION

pgfin.pk006.c7 normalized chicken fat cDNA library Gallus gallus cDNA clone pgfin.pk006.c7 5' similar to emb|X54094.1|GGF1L Gallus gallus endogenous virus-21 JF1L-1 DNA sequence, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Gallus gallus (chicken)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Larry A. Cogburn

University of Delaware

Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-1335

Fax: 302-831-2822

Email: cogburn@udel.edu, www.chickest.udel.edu.

## FEATURES

## source

1..377  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="pgfin.pk006.c7"  
/sex="Male and Female"  
/tissue\_type="fat"  
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/clone\_lib="normalized chicken fat cDNA library"  
/note="Vector: pSPORT1"

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Best Local Similarity 90.2%; Pred. No. 2.7e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCCTATCTGAGGGACCTAGGTTGCTTTAGCGGAAAGCGGGCTTCGGTTGTACCGGT 209

Db 76 GCTTGACTGAGGGGACCTAGTATGATATAGCGGCGGGCTTCGGTTGTACCGGT 135

Qy 210 TAGGAGTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
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 Db 136 TAGAGTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGTAGTCTA 195  
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 Qy 270 TAT 272  
 ||  
 Db 196 AAT 198

RESULT 5  
 CF250631  
 LOCUS esa018 907 Eimeiria tenella-infected caecal tonsil Gallus gallus EST 07-AUG-2003  
 DEFINITION cDNA, mRNA sequence.  
 ACCESSION CF250631.1 GI:33483886  
 VERSION CF250631  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 414).  
 AUTHORS Wittzell,H., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J.,  
 Chausse,A.M. and Zoorob,R.  
 TITLE A collection of chicken ESTs from activated immune cells  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Zoorob R  
 UPR 1983  
 CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
 Tel: 33 1 49 58 35 00  
 Fax: 33 1 49 58 33 81  
 Email: zoorob@vjf.cnrs.fr.

FEATURES  
 source  
 1. .414  
 /organism="Gallus gallus"  
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 /db\_xref="taxon:9031"  
 /clone\_lib="Eimeiria tenella-infected caecal tonsil"  
 /note="Organ: Caecal tonsil; Vector: pTriplex2"

ORIGIN  
 Query Match 19.8%; Score 103.8; DB 14; Length 414;  
 Best local Similarity 90.2%; Pred. No. 2.8e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGGCGGAAAGCGGGCTTCGGTTGTACGCGGT 209  
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 Db 113 GCTTGACTGAGGGGACCATAGTATGTATAGGCGGAAAGCGGGCTTCGGTTGTACGCGGT 172  
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 Qy 210 TAGGAGTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
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 Db 173 TAGAGTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGTAGTCTA 232  
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 Qy 270 TAT 272  
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 Db 233 AAT 235

RESULT 6  
 CF250926  
 LOCUS esa018 907 Eimeiria tenella-infected caecal tonsil Gallus gallus EST 07-AUG-2003  
 DEFINITION cDNA, mRNA sequence.  
 ACCESSION CF250926  
 VERSION CF250926.1 GI:33484181  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 454).  
 AUTHORS Wittzell,H., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J.,  
 Chausse,A.M. and Zoorob,R.  
 TITLE A collection of chicken ESTs from activated immune cells  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Zoorob R  
 UPR 1983  
 CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
 Tel: 33 1 49 58 35 00  
 Fax: 33 1 49 58 33 81  
 Email: zoorob@vjf.cnrs.fr.

FEATURES  
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 1. .454  
 /organism="Gallus gallus"  
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 /clone\_lib="Eimeiria tenella-infected caecal tonsil"  
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 Best local Similarity 90.2%; Pred. No. 2.9e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGGCGGAAAGCGGGCTTCGGTTGTACGCGGT 209  
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 Db 123 GCTTGACTGAGGGGACCATAGTATGTATAGGCGGAAAGCGGGCTTCGGTTGTACGCGGT 182  
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 Qy 210 TAGGAGTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
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 Db 183 TAGGAGTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGTAGTCTA 242  
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 Qy 270 TAT 272  
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 Db 243 AAT 245

RESULT 7  
 BUI23326  
 LOCUS BUI23326 648 bp mRNA linear EST 25-NOV-2002  
 DEFINITION 603147220F1 CSEQCHL18 Gallus gallus cDNA clone CHEST1486 5', mRNA  
 sequence.  
 ACCESSION BUI23326  
 VERSION BUI23326.1 GI:25333962  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 648)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers

FEATURES  
 source  
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 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"

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/clone="CHESTR1496"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHL18"
/note="Organ: small intestine; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI; Modification of
pBluescript II KS(+) [Stratagene] vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
containing BspI and BamHI sites
[5'ggcgcgtgagcccgatccgaaaaag]
[5'aattcttttggatccgggtgcagc]"

ORIGIN
Query Match 19.8%; Score 103.8; DB 13; Length 648;
Best Local Similarity 90.2%; Pred. No. 3.4e-21;
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGCGGAAAAGCGGGCTTCGGTTGTACGGGT 209
Db 337 GCTTGACTGAGGGGACCTAGTATGTATAGCGGAGGCGGGCTTCGGTTGTACGGGT 396
QY 210 TAGAGTCCCTCAGATATAGTATTCGCTTTTGCATAGGAGGGGAAAATGTAGTCT 269
Db 397 TAGAGTCCCTCAGATATAGTATTCGCTTTTGCATAGGAGGGGAAAATGTAGTCTA 456
QY 270 TAT 272
Db 457 AAT 459

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RESULT 8
LOCUS BU338428 661 bp mRNA linear EST 28-NOV-2002
DEFINITION 603513043F1 CSEQCHN66 Gallus gallus CDNA clone CHEST449e12 5', mRNA
sequence.
ACCESSION BU338428
VERSION BU338428.1 GI:25846429
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 661)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .661
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST449e12"
/dev_stage="16 day embryo"
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/note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methyated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

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ORIGIN
Query Match 19.8%; Score 103.8; DB 13; Length 661;
Best Local Similarity 90.2%; Pred. No. 3.4e-21;
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGCGGAAAAGCGGGCTTCGGTTGTACGGGT 209
Db 351 GCTTGACTGAGGGGACCTAGTATGTATAGCGGAGGCGGGCTTCGGTTGTACGGGT 410
QY 210 TAGAGTCCCTCAGATATAGTATTCGCTTTTGCATAGGAGGGGAAAATGTAGTCT 269
Db 411 TAGAGTCCCTCAGATATAGTATTCGCTTTTGCATAGGAGGGGAAAATGTAGTCTA 470
QY 270 TAT 272
Db 471 AAT 473

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RESULT 9
LOCUS BU452326 668 bp mRNA linear EST 29-NOV-2002
DEFINITION 603768694F1 CSEQRBN14 Gallus gallus CDNA clone CHEST698124 5', mRNA
sequence.
ACCESSION BU452326
VERSION BU452326.1 GI:25941637
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 668)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .668
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST698124"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBN14"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site 1:

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ECORI, Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcorI, size-selected, and cloned into the NotI and EcorI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 668;  
Best Local Similarity 90.2%; Pred. No. 3.4e-21;  
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DB 360 GCTTGACTGAGGGGACCATAGTATGTATAGGCGGAAAGCGGGGCTTCGGTTGTACGGGT 419  
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QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTAGGAGGGGGAATGTAGTCT 269  
|||  
DB 420 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTAGGAGGGGGAATGTAGTCTA 479  
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QY 270 TAT 272  
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DB 480 AAT 482

## RESULT 10

BU104175  
LOCUS BU104175.1 673 bp mRNA linear EST 25-NOV-2002  
DEFINITION 603004302F1 CSPQCHL01 Gallus gallus cDNA clone CHEST19d2 5', mRNA  
sequence.  
ACCESSION BU104175  
VERSION BU104175.1 GI:25305018  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 673)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..673  
/organism="Gallus gallus"  
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Site\_1: EcorI; Site\_2: NotI; Modification of pBluescript

II KS(+). [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcorI. Ligate in double stranded adaptor containing BsgI and BamHI sites  
[5'ggcgcgctgcagcccgatccgaaaaag]  
[5'aattcttttctggatccggggtgcagc]"

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 673;  
Best Local Similarity 90.2%; Pred. No. 3.5e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGGCGGAAAGCGGGGCTTCGGTTGTACGGGT 209  
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DB 344 GCTTGACTGAGGGGACCATAGTATGTATAGGCGGAAAGCGGGGCTTCGGTTGTACGGGT 403  
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QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTAGGAGGGGGAATGTAGTCT 269  
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DB 404 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTAGGAGGGGGAATGTAGTCTA 463  
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QY 270 TAT 272  
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DB 464 AAT 466

## RESULT 11

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DEFINITION 603671572F1 CSEQRBL07 Gallus gallus cDNA clone CHEST616p.18 5', mRNA  
sequence.  
ACCESSION BU417201  
VERSION BU417201.1 GI:25909872  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 728)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..728  
/organism="Gallus gallus"  
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/clone\_lib="CSEQRBL07"  
/note="Organ: pancreas; Vector: pBluescript II KS(+);  
Site\_1: EcorI; Site\_2: NotI; Modification of pBluescript  
II KS(+). [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al.

U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites  
 [5'ggcgcgtgcagcccgatccgaaagaaag]  
 [5'aattcttttttcggatccgggctgcacgc]

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 728;  
 Best Local Similarity 90.2%; Pred. No. 3.6e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTAGGCGAAAGCGGGGCTTCGCTTTGACGCGGT 209  
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 DB 523 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAAGCGGGGCTTCGCTTTGACGCGGT 582  
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QY 210 TAGGAGTCCCTCAGGATATAGTGTTCGCTTTTGCATAGGAGGCGGAAATGTAGTCT 269  
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 DB 583 TAGGAGTCCCTCAGGATATAGTGTTCGCTTTTGCATAGGAGGCGGAAATGTAGTCT 642  
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QY 270 TAT 272  
 |||  
 DB 643 AAT 645

RESULT 12  
 BU4705810  
 LOCUS 741 bp mRNA linear EST 28-NOV-2002  
 DEFINITION 603489965F1 CSQCHN63 Gallus gallus cDNA clone CHEST390b18 5', mRNA sequence.  
 ACCESSION BU325810  
 VERSION BU325810.1 GI:25833811  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 741)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
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 /organism="Gallus gallus"  
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 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST390b18"  
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 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN63"  
 /note="Organ: heads; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

## FEATURES

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 /organism="Gallus gallus"  
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 /clone\_lib="CSEQCHN63"  
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## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 741;  
 Best Local Similarity 90.2%; Pred. No. 3.6e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTAGGCGAAAGCGGGGCTTCGCTTTGACGCGGT 209  
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 DB 578 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAAGCGGGGCTTCGCTTTGACGCGGT 637  
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QY 210 TAGGAGTCCCTCAGGATATAGTGTTCGCTTTTGCATAGGAGGCGGAAATGTAGTCT 269  
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 DB 638 TAGGAGTCCCTCAGGATATAGTGTTCGCTTTTGCATAGGAGGCGGAAATGTAGTCT 697  
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QY 270 TAT 272  
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 DB 698 AAT 700

## RESULT 13

BU470589  
 LOCUS 777 bp mRNA linear EST 30-NOV-2002  
 DEFINITION 603760251F1 CSQREN21 Gallus gallus cDNA clone CHEST677f14 5', mRNA sequence.  
 ACCESSION BU470589  
 VERSION BU470589.1 GI:25964166  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 777)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..777  
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 /strain="Layer"  
 /db\_xref="taxon:9031"  
 /clone="CHEST677f14"  
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 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQREN21"  
 /note="Organ: ovary; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

## FEATURES

## source

1..777  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:9031"  
 /clone="CHEST677f14"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQREN21"  
 /note="Organ: ovary; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

(1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 777;  
Best Local Similarity 90.2%; Pred. No. 3.7e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGGTGTGTTTAGGCGAAAGCGGGGCTTCGGTTGTACGGGT 209  
|||  
DB 558 GCTTGACTGAGGGAGCCATAGTATGTATAGCGAAGCGGGGCTTCGGTTGTACGGGT 617  
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QY 210 TAGGAGTCCCTCAGGATATAGTGTTCGTTTCATAGGAGGGGAAATGTAGTCT 269  
|||

DB 618 TAGGAGTCCCTCAGGATATAGTGTTCGTTTCATAGGAGGGGAAATGTAGTCA 677  
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QY 270 TAT 272  
|||

DB 678 AAT 680  
|||

## RESULT 14

BU444255  
LOCUS BU444255 784 bp mRNA linear EST 29-NOV-2002  
DEFINITION 603767471F1 CSEQBN13 Gallus gallus cDNA clone CHEST695n18 5', mRNA  
sequence.  
ACCESSION BU444255  
VERSION BU444255.1 GI:25933566  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 784)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

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/note="Organ: ovary; Vector: pBluescript II KS(+); Site\_1:  
EcORI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcORI, size-selected, and cloned into the NotI and EcORI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer

reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 784;  
Best Local Similarity 90.2%; Pred. No. 3.7e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGGTGTGTTTAGGCGAAAGCGGGGCTTCGGTTGTACGGGT 209  
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DB 482 GCTTGACTGAGGGAGCCATAGTATGTATAGCGAAGCGGGGCTTCGGTTGTACGGGT 541  
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QY 210 TAGGAGTCCCTCAGGATATAGTGTTCGTTTCATAGGAGGGGAAATGTAGTCT 269  
|||

DB 542 TAGGAGTCCCTCAGGATATAGTGTTCGTTTCATAGGAGGGGAAATGTAGTCA 601  
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QY 270 TAT 272  
|||

DB 602 AAT 604  
|||

## RESULT 15

BU312414  
LOCUS BU312414 793 bp mRNA linear EST 28-NOV-2002  
DEFINITION 603541447F1 CSEQCHN61 Gallus gallus cDNA clone CHEST51ml2 5', mRNA  
sequence.  
ACCESSION BU312414  
VERSION BU312414.1 GI:25820415  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1. .793  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST51ml2"  
/sex="Female"  
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/lab\_host="DH10B"  
/clone\_lib="CSEQCHN61"  
/note="Organ: heart; Vector: pBluescript II KS(+); Site\_1:  
EcORI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcORI, size-selected, and cloned into the NotI and EcORI  
compatible sites of a custom Modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 793;  
 Best Local Similarity 90.2%; Pred. No. 3.7e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGGCTTCGGTTGTACGCGGT 209  
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 Db 495 GCTTGACTGAGGGACCATAGTATGATAGGCGAAGCGGGGCTTCGGTTGTACGCGGT 554  
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QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
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QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
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 Db 539 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCT 598  
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QY 270 TAT 272  
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 Db 599 AAT 601

RESULT 16  
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 DEFINITION 603110079F1 CSEQCHL12 Gallus gallus cDNA clone ChEST55m20 5', mRNA  
 sequence.

ACCESSION BUI07637  
 VERSION BUI07637.1 GI:25310244  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus (chicken)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 801)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..801  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
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 /note="Organ: heart; Vector: pBluescript II KS(+); Site 1:  
 EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
 [Stratagene] vector to accommodate cDNA produced with the  
 T-timed protocol (construction of uni-directionally  
 cloned cDNA libraries from messenger RNA for improved 3'  
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
 Ligate in double stranded adaptor containing BspI and  
 BamHI sites [5'ggcgcgtgcagcccgatccgaaaaag]  
 [5'aattcttttttcggatccgggtcagc]"

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 801;  
 Best Local Similarity 90.2%; Pred. No. 3.7e-21;  
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QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGGCTTCGGTTGTACGCGGT 209  
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 Db 495 GCTTGACTGAGGGACCATAGTATGATAGGCGAAGCGGGGCTTCGGTTGTACGCGGT 554  
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QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
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 Db 555 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCT 614  
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QY 270 TAT 272  
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 Db 615 AAT 617

RESULT 17  
 BUI14728  
 LOCUS 834 bp mRNA linear EST 28-NOV-2002  
 DEFINITION 603541055F1 CSEQCHN61 Gallus gallus cDNA clone ChEST510m14 5', mRNA  
 sequence.

ACCESSION BUI14728  
 VERSION BUI14728  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 834)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..834  
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 /clone\_lib="CSEQCHN61"  
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 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 834;  
 Best Local Similarity 90.2%; Pred. No. 3.8e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGGCTTCGGTTGTACGCGGT 209



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Db      529 GCTTGACTGAGGGACCATAGATATAGTATAGGCGAAAGCGGGCTTCGGTTGTACCGGT 588
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Db      589 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCA 648
QY      270 TAT 272
Db      649 AAT 651

RESULT 19
LOCUS   BU413305
DEFINITION 603155306F1 CSEQRL05 Gallus gallus cDNA clone CHEST16812 5', mRNA
sequence.
ACCESSION BU413305
VERSION   BU413305.1 GI:25905976
KEYWORDS EST.
SOURCE   Gallus gallus (chicken)
ORGANISM Gallus gallus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 835)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
          Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE    A Comprehensive Collection of Chicken cDNAs
JOURNAL  Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED  12445392
COMMENT  Contact: Simon Hubbard
          Department of Biomolecular Sciences
          University of Manchester Institute of Science and Technology
          (UMIST)
          PO Box 88, Manchester, M60 1QD, UK
          Tel: 01612008930
          Fax: 01612360409
          Email: Simon.Hubbard@umist.ac.uk.

FEATURES
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                /clone_lib="CSEQRL05"
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                EcoRI; Site 2: NotI; Modification of pBluescript II KS(+):
                [Stratagene] vector to accommodate cDNA produced with the
                T-trimmed protocol (Construction of uni-directionally
                cloned cDNA libraries from messenger RNA for improved 3'
                end DNA sequencing by Glenn Fu, et al. U.S. Patent #
                6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
                Ligate in double stranded adaptor containing BspI and
                BamHI sites [5'ggccgctgcagccgccgagtcacgaaagag]
                [5'aattcttttttcggatccggggtgcagc]"

ORIGIN
Query Match      19.8%; Score 103.8; DB 13; Length 835;
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Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      150 GCGTATCTGAGGGAGCTAGGGTGTGTTTAGGCGAAAGCGGGCTTCGGTTGTACCGGT 209
Db      532 GCTTGACTGAGGGACCATAGATATAGTATAGGCGAAAGCGGGCTTCGGTTGTACCGGT 591
QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCT 269

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Db      592 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCA 651
QY      270 TAT 272
Db      652 AAT 654

RESULT 19
LOCUS   BU354615
DEFINITION 603473642F1 CSEQHN70 Gallus gallus cDNA clone CHEST353d11 5', mRNA
sequence.
ACCESSION BU354615
VERSION   BU354615.1 GI:25862616
KEYWORDS EST.
SOURCE   Gallus gallus (chicken)
ORGANISM Gallus gallus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 859)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
          Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE    A Comprehensive Collection of Chicken cDNAs
JOURNAL  Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED  12445392
COMMENT  Contact: Simon Hubbard
          Department of Biomolecular Sciences
          University of Manchester Institute of Science and Technology
          (UMIST)
          PO Box 88, Manchester, M60 1QD, UK
          Tel: 01612008930
          Fax: 01612360409
          Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source          1..859
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                /strain="White Leghorn, HiseX"
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                /notes="Organ: hearts; Vector: pBluescript II KS(+);
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                methylated C in the first strand synthesis reaction.
                Following this first strand reaction, double-stranded cDNA
                was blunted, ligated to NotI adapters, digested with
                EcoRI, size-selected, and cloned into the NotI and EcoRI
                compatible sites of a custom modified MCS of the
                pBluescript (KS+) vector. The library was normalized in 2
                rounds using conditions adapted from Soares et al., PNAS
                (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                (1996): 791, except that a significantly longer
                reannealing hybridization was used."

ORIGIN
Query Match      19.8%; Score 103.8; DB 13; Length 859;
Best Local Similarity 90.2%; Pred. No. 3.8e-21;
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      150 GCGTATCTGAGGGAGCTAGGGTGTGTTTAGGCGAAAGCGGGCTTCGGTTGTACCGGT 209
Db      549 GCTTGACTGAGGGACCATAGATATAGTATAGGCGAAAGCGGGCTTCGGTTGTACCGGT 608
QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCT 269
Db      609 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCA 668

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QY      270 TAT 272
Db      ||
        569 AAT 671

RESULT 20
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LOCUS      604129304F1 CSEQBN37 Gallus gallus cDNA clone ChEST953h2 5', mRNA
DEFINITION      sequence.
ACCESSION      BU490656
VERSION      604129304F1 CSEQBN37 Gallus gallus (chicken)
KEYWORDS      EST.
SOURCE      Gallus gallus
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 725)
AUTHORS      Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
              Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
              A Comprehensive Collection of Chicken cDNAs
              Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL      Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE      22335534
PUBMED      12445392
COMMENT      Contact: Simon Hubbard
              Department of Biomolecular Sciences
              University of Manchester Institute of Science and Technology
              (UMIST)
              PO Box 88, Manchester, M60 1QD, UK
              Tel: 01612008930
              Fax: 01612360409
              Email: Simon.Hubbard@umist.ac.uk.
              Location/Qualifiers
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                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand reaction, double-stranded cDNA
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN
Query Match      19.7%; Score 103; DB 13; Length 725;
Best Local Similarity      91.6%; Pred. No. 6.3e-21;
Matches 109; Conservative      0; Mismatches 10; Indels      0; Gaps      0;

QY      150 GCCTACTGAGGGGACTAGAGTGTGTTTAGCGAAGAGCGGGCTTCGGTTGTACGCGT 209
Db      |||
        558 GTTGTACTGAGGGACCATAGTATGATATAGCGAAGAGCGGGCTTCGGTTGTACGCGT 617

QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 268
Db      |||
        618 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 676

Query Match      19.7%; Score 103; DB 13; Length 725;
Best Local Similarity      91.6%; Pred. No. 6.3e-21;
Matches 109; Conservative      0; Mismatches 10; Indels      0; Gaps      0;

QY      150 GCCTACTGAGGGGACTAGAGTGTGTTTAGCGAAGAGCGGGCTTCGGTTGTACGCGT 209
Db      |||
        558 GTTGTACTGAGGGACCATAGTATGATATAGCGAAGAGCGGGCTTCGGTTGTACGCGT 617

QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 268
Db      |||
        618 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 676

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RESULT 21
BU132452      773 bp mRNA linear EST 25-NOV-2002
LOCUS      603120761F1 CSEQCHL22 Gallus gallus cDNA clone ChEST82i15 5', mRNA
DEFINITION      sequence.
ACCESSION      BU132452
VERSION      BU132452.1 GI:25344537
KEYWORDS      EST.
SOURCE      Gallus gallus (chicken)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 773)
AUTHORS      Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
              Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
              A Comprehensive Collection of Chicken cDNAs
              Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL      Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE      22335534
PUBMED      12445392
COMMENT      Contact: Simon Hubbard
              Department of Biomolecular Sciences
              University of Manchester Institute of Science and Technology
              (UMIST)
              PO Box 88, Manchester, M60 1QD, UK
              Tel: 01612008930
              Fax: 01612360409
              Email: Simon.Hubbard@umist.ac.uk.
              Location/Qualifiers
FEATURES             source
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                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
                     /db_xref="taxon:9031"
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                     /lab_host="DH10B"
                     /clone_lib="CSEQCHL22"
                     /note="Organ: heads; Vector: pBluescript II KS(+); Site 1:
                     EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
                     [Stratagene] vector to accommodate cDNA produced with the
                     T-trimmed protocol (Construction of uni-directionally
                     cloned cDNA libraries from messenger RNA for improved 3'
                     end DNA sequencing by Glenn Fu, et al. U.S. Patent #
                     6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
                     Ligate in double stranded adaptor containing BspI and
                     BamHI sites [5'ggccggtgcagccgcggtatccgaaaaag]
                     [5'aattcttttttggatccggggtgcagcg]"
ORIGIN
Query Match      19.5%; Score 102.2; DB 13; Length 773;
Best Local Similarity      89.4%; Pred. No. 1.2e-20;
Matches 110; Conservative      0; Mismatches 13; Indels      0; Gaps      0;

QY      150 GCCTACTGAGGGGACTAGAGTGTGTTTAGCGAAGAGCGGGCTTCGGTTGTACGCGT 209
Db      |||
        513 GTTGTACTGAGGGGACCATAGTATGATATAGCGAAGAGCGGGCTTCGGTTGTACGCGT 572

QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 269
Db      |||
        573 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 632

QY      270 TAT 272
Db      ||
        633 AAT 635

RESULT 22
BU343905      732 bp mRNA linear EST 28-NOV-2002
LOCUS      603525493F1 CSEQCHN68 Gallus gallus cDNA clone ChEST471i24 5', mRNA
DEFINITION      sequence.
ACCESSION      BU343905

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VERSION      BU343905.1  GI:25851906
KEYWORDS     EST
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
REFERENCE    1 (bases 1 to 732)
AUTHORS      Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
              Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE        A Comprehensive Collection of Chicken cDNAs
JOURNAL      Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE      22335534
PUBMED       12445392
COMMENT      Contact: Simon Hubbard
              Department of Biomolecular Sciences
              University of Manchester Institute of Science and Technology
              (UMIST)
              PO Box 88, Manchester, M60 1QD, UK
              Tel: 01612008930
              Fax: 01612360409
              Email: Simon.Hubbard@umist.ac.uk.
              Location/Qualifiers
FEATURES     source
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                /mol_type="mRNA"
                /strain="Compton Line 151"
                /db_xref="taxon:9031"
                /clone="CHST471i24"
                /sex="Female"
                /tissue_type="cerebellum"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="CSEQCHM68"
                /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
              EcoRI; Site 2: NotI; This normalized library was
              constructed from 1 million independent clones. cDNA
              synthesis was initiated using an oligo(dT) primer, using
              methylated C in the first strand synthesis reaction.
              Following this first strand reaction, double-stranded cDNA
              was blunted, ligated to NotI adapters, digested with
              EcoRI, size-selected, and cloned into the NotI and EcoRI
              compatible sites of a custom modified MCS of the
              pBluescript (KS+) vector. The library was normalized in 2
              rounds using conditions adapted from Soares et al., PNAS
              (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
              (1996): 791, except that a significantly longer
              reannealing hybridization was used."
ORIGIN
Query Match      19.2%; Score 100.6; DB 13; Length 732;
Best Local Similarity 88.6%; Pred. No. 3.6e-20;
Matches 109; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 150 GGGTATCTGAGGGGACTAGGTGTGTTTAGGCGAAAGCGGGGCTTCGGTTGTACGGGT 209
    |||
Db 425 GTTTGACTGAGGGGACCATAGTATGTATAGCGGCAAGCGGGGCTTCGGTTGTACGGGT 484
QY 210 TAGGAGTCCCTTCAGGATATAGTATGCTTTGCGTTTGCATAGGGAGGGGGAATGTAGTCT 269
    |||
Db 485 TAGGAGTCCCTTCAGGATATAGTATGCTTTGCGTTTGCATAGGGAGGGGGAATGTAGTCTA 544
QY 270 TAT 272
    |||
Db 545 AAT 547

RESULT 23
BU309030
LOCUS      603538660F1 CSEQCHN60 Gallus gallus cDNA clone CHEST504g16 5', mRNA
DEFINITION
sequence.
ACCESSION  BU309030

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VERSION      BU309030.1  GI:25817031
KEYWORDS     EST
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
REFERENCE    1 (bases 1 to 744)
AUTHORS      Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
              Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE        A Comprehensive Collection of Chicken cDNAs
JOURNAL      Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE      22335534
PUBMED       12445392
COMMENT      Contact: Simon Hubbard
              Department of Biomolecular Sciences
              University of Manchester Institute of Science and Technology
              (UMIST)
              PO Box 88, Manchester, M60 1QD, UK
              Tel: 01612008930
              Fax: 01612360409
              Email: Simon.Hubbard@umist.ac.uk.
              Location/Qualifiers
FEATURES     source
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                /organism="Gallus gallus"
                /mol_type="mRNA"
                /strain="Compton Line 151"
                /db_xref="taxon:9031"
                /clone="CHST504g16"
                /sex="Female"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="CSEQCHN60"
                /note="Organ: heart; Vector: pBluescript II KS(+); Site_1:
              EcoRI; Site 2: NotI; This normalized library was
              constructed from 1 million independent clones. cDNA
              synthesis was initiated using an oligo(dT) primer, using
              methylated C in the first strand synthesis reaction.
              Following this first strand reaction, double-stranded cDNA
              was blunted, ligated to NotI adapters, digested with
              EcoRI, size-selected, and cloned into the NotI and EcoRI
              compatible sites of a custom modified MCS of the
              pBluescript (KS+) vector. The library was normalized in 2
              rounds using conditions adapted from Soares et al., PNAS
              (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
              (1996): 791, except that a significantly longer
              reannealing hybridization was used."
ORIGIN
Query Match      19.2%; Score 100.6; DB 13; Length 744;
Best Local Similarity 88.6%; Pred. No. 3.6e-20;
Matches 109; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 150 GGGTATCTGAGGGGACTAGGTGTGTTTAGGCGAAAGCGGGGCTTCGGTTGTACGGGT 209
    |||
Db 223 GTTTGACTGAGGGGACCATAGTATGTATAGCGGCAAGCGGGGCTTCGGTTGTACGGGT 282
QY 210 TAGGAGTCCCTTCAGGATATAGTATGCTTTGCGTTTGCATAGGGAGGGGGAATGTAGTCT 269
    |||
Db 283 TAGGAGTCCCTTCAGGATATAGTATGCTTTGCGTTTGCATAGGGAGGGGGAATGTAGTCTA 342
QY 270 TAT 272
    |||
Db 343 AAT 345

RESULT 24
BU143329
LOCUS      603230107F1 CSEQCHL26 Gallus gallus cDNA clone CHEST224m2 5', mRNA
DEFINITION
sequence.
ACCESSION  BU143329
VERSION    BU143329.1  GI:25359668

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KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE 22335534

PUBMED 12445392

COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
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Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..1012  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:9031"  
/clone="CHEST24m2"  
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/lab\_host="DH10B"  
/clone\_lib="CSQRBN37"  
/notes="Organ: heart; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol. (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BglI and BamHI sites [5'ggcgcgtgcagcccgatcgaaaaaag] [5'aattcttttttcggatccgggtgcagc]"

ORIGIN  
Query Match 19.2%; Score 100.6; DB 13; Length 1012;  
Best Local Similarity 88.6%; Pred. No. 4.1e-20;  
Matches 109; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGTGTGTTAGGCGAAAGCGGGCTTCGGTTGTACGGGT 209  
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Db 590 GCTTGACTGAGGGGACCAATGTATGTATAGGCGAAAGCGGGCTTCGGTTGTACGGGT 649  
|||

QY 210 TAGGAGTCCCTCAGCATATAGTATGTTGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
|||  
Db 650 TAGGAGTCCCTCAGCATATAGTATGTTGCTTTTGCATAGGAGTCCGGAATGTAGTCT 709  
|||

QY 270 TAT 272  
|||  
Db 710 AAT 712

RESULT 25  
BU490989  
LOCUS 604127967F1 CSQRBN37 Gallus gallus cDNA clone CHEST950e17 5', mRNA  
DEFINITION sequence.

ACCESSION BU490989  
VERSION BU490989.1 GI:25984566  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.  
1 (bases 1 to 695)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
PUBMED 12445392

COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..695  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
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/sex="Male and female"  
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/lab\_host="DH10B"  
/clone\_lib="CSQRBN37"  
/notes="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN  
Query Match 18.2%; Score 95; DB 13; Length 695;  
Best Local Similarity 91.0%; Pred. No. 2e-18;  
Matches 101; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGTGTGTTAGGCGAAAGCGGGCTTCGGTTGTACGGGT 209  
|||  
Db 581 GCTTGACTGAGGGGACCAATGTATGTATAGGCGAAAGCGGGCTTCGGTTGTACGGGT 640  
|||

QY 210 TAGGAGTCCCTCAGCATATAGTATGTTGCTTTTGCATAGGAGGGGGA 260  
|||  
Db 641 TAGGAGTCCCTCAGCATATAGTATGTTGCTTTTGCATAGGAGGGGGA 691  
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RESULT 26  
CB016682  
LOCUS 270 bp mRNA linear EST 10-JAN-2003  
DEFINITION pgnic.pk013.d10 Chicken lymphoid cDNA library (pgnic) Gallus gallus cDNA clone pgnic.pk013.d10 5' similar to gb|AF013304.1 Avian leukosis virus strain av-3, complete genome, mRNA sequence.

ACCESSION CB016682  
VERSION CB016682.1 GI:27591418  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 270)  
Morgan, R.W. and Burnside, J.  
Chicken ESTs from lymphoid tissue

JOURNAL  
COMMENT

Unpublished (2002)  
Contact: Robin W. Morgan  
University of Delaware  
Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1341  
Fax: 302-831-2822  
Email: morgan@udel.edu, www.chickent.udel.edu.  
Location/Qualifiers

## FEATURES

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/clone\_lib="Chicken lymphoid cDNA library (pgnic)"  
/note="Vector: pcWVSPORT 6"

## ORIGIN

Query Match 17.9%; Score 93.6; DB 14; Length 270;  
Best Local Similarity 84.7%; Pred. No. 3.8e-18;  
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 150 GCGTATCTGAGGGAGTCTAGGCTGTCTTTAGGCGCAAAAGCGGGCTTCGGTTGTACGGCGT 209  
Db 120 GCTTGACTGAGGGAGCACATAGTATGTATAGGCGCAAAAGCGGGCTTCGGTTGTACGGCGT 179  
QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGCAATGATCT 269  
Db 180 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGCAATGATCT 239  
QY 270 TATG 273  
Db 240 GAGG 243

## RESULT 27

BU263560  
LOCUS BU263560 669 bp mRNA linear EST 26-NOV-2002  
DEFINITION 603014517F1 CSEQCHN52 Gallus gallus cDNA clone CHEST806a6 5', mRNA  
sequence.  
ACCESSION BU263560  
VERSION BU263560.1 GI:25533091  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 669)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..669  
/organism="Gallus gallus"  
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## /lab\_host="DH10B"

/clone\_lib="CSEQCHN52"  
/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:  
ECORI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunt-ended, ligated to NotI adapters, digested with  
ECORI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 17.9%; Score 93.4; DB 13; Length 669;  
Best Local Similarity 90.1%; Pred. No. 6.3e-18;  
Matches 100; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 150 GCGTATCTGAGGGAGTCTAGGCTGTCTTTAGGCGCAAAAGCGGGCTTCGGTTGTACGGCGT 209  
Db 559 GCTTGACTGAGGGAGCACATAGTATGTATAGGCGCAAAAGCGGGCTTCGGTTGTACGGCGT 618  
QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGCA 260  
Db 619 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGCA 669

## RESULT 28

BU356927  
LOCUS BU356927 810 bp mRNA linear EST 28-NOV-2002  
DEFINITION 603475272F1 CSEQCHN70 Gallus gallus cDNA clone CHEST357p17 5', mRNA  
sequence.  
ACCESSION BU356927  
VERSION BU356927.1 GI:25864928  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 810)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers

FEATURES  
source

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/clone\_lib="CSEQCHN70"  
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Site 1: EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using

methyated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 17.7%; Score 92.8; DB 13; Length 810;  
Best Local Similarity 89.5%; Pred. No. 1.1e-17;  
Matches 111; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 150 GCGTATCTGAGGGGACTAGGCTGTGTAGGCGAAGCGGGCTTCGGTTGTACGCGGT 209  
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Db 489 GCTTGACTGAGGGGACCTAGTATGATAGGCGAAGCGGGCTTCGGTTGTACGCGGT 548  
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QY 210 TAGGAGTCCCTCAGGATATAGT-AGTTTCGCTTTTCATAGGAGGGGGAATGTAGTC 268  
|||  
Db 549 TAGGAGTCCCTCAGGATATAGT-AGTTTCGCTTTTCATAGGAGGGGGAATGTAGTC 508  
|||

QY 269 TTAT 272  
||  
Db 609 AAAT 612

RESULT 29  
BU492375  
LOCUS  
DEFINITION 60413252F1 CSEQRN37 Gallus gallus cDNA clone ChEST961g13 5', mRNA  
sequence.  
ACCESSION BU492375  
VERSION BU492375.1 GI:25985952  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 623)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1. .623  
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/lab\_host="DH10B"  
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/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methyated C in the first strand synthesis reaction."

Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 16.9%; Score 88.2; DB 13; Length 623;  
Best Local Similarity 88.1%; Pred. No. 2.6e-16;  
Matches 96; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGCTGTGTAGGCGAAGCGGGCTTCGGTTGTACGCGGT 209  
|||  
Db 509 GCTTGACTGAGGGGACCTAGTATGATAGGCGAAGCGGGCTTCGGTTGTACGCGGT 568  
|||

QY 210 TAGGAGTCCCTCAGGATATAGT-AGTTTCGCTTTTCATAGGAGGGG 258  
|||  
Db 569 TAGGAGTCCCTCAGGATATAGT-AGTTTCGCTTTTCATAGGAGGGG 617  
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RESULT 30  
BU404431  
LOCUS  
DEFINITION 604138647F1 CSEQRN59 Gallus gallus cDNA clone ChEST967n11 5', mRNA  
sequence.  
ACCESSION BU404431  
VERSION BU404431.1 GI:25773487  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 418)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
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Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
1. .418  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
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/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methyated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 16.8%; Score 88; DB 13; Length 418;  
Best Local Similarity 90.4%; Pred. No. 2.6e-16;  
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGCTTCGGTTGTACCGGT 209  
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Db 495 GCTTGACTAGGGGACCACTAGTATGATAGCGGAAAGCGGGCTTCGGTTGTACCGGT 374  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGGA 253  
|||

Db 375 TAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGGA 418  
|||

RESULT 31  
BU490064  
LOCUS 598 bp mRNA linear EST 30-NOV-2002  
DEFINITION 604132030F1 CSEQBN37 Gallus gallus cDNA clone ChEST960k8 5', mRNA sequence.

ACCESSION BU490064  
VERSION BU490064.1 GI:25983641  
KEYWORDS EST.

SOURCE Gallus gallus (chicken)  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 598)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J., A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
PUBMED 12445392

COMMENT Contact: Simon Hubbard  
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Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

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Location/Qualifiers  
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/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQBN37"

/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 16.8%; Score 88; DB 13; Length 598;  
Best Local Similarity 90.4%; Pred. No. 3e-16;  
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGCTTCGGTTGTACCGGT 209  
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Db 495 GCTTGACTAGGGGACCACTAGTATGATAGCGGAAAGCGGGCTTCGGTTGTACCGGT 554  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGGA 253  
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Db 555 TAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGGA 598  
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RESULT 32  
BU487895  
LOCUS 773 bp mRNA linear EST 30-NOV-2002  
DEFINITION 604126611F1 CSEQBN36 Gallus gallus cDNA clone ChEST946f3 5', mRNA sequence.

ACCESSION BU487895  
VERSION BU487895.1 GI:25981472  
KEYWORDS EST.

SOURCE Gallus gallus (chicken)  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 773)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J., A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
PUBMED 12445392

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## FEATURES

source  
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/organism="Gallus gallus"  
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/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQBN36"

/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 16.8%; Score 88; DB 13; Length 773;  
Best Local Similarity 90.4%; Pred. No. 3.3e-16;  
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGCTTCGGTTGTACCGGT 209  
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Db      502  GCTTGACTGAGGCGACCATAGTATGATAGCGGAAGGCGGGCTTCGGTGTACGCGGT 561
Qy      210  TAGGAGTCCCTCAGCATATAGTATGCTTTCGTTTGCATAGGGA 253
Db      562  TAGGAGTCCCTCAGCATATAGTATGCTTTCGTTTGCATAGGGA 605

RESULT 33
BU474299/c
LOCUS   BU474299
DEFINITION BU474299.1 CSEQREN21 Gallus gallus CDNA clone CHEST258524 5', mRNA
sequence.
ACCESSION BU474299
VERSION   BU474299
KEYWORDS  EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Gallus gallus

REFERENCE
AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
           Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE     A Comprehensive Collection of Chicken cDNAs
JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE   22335534
PUBMED    12445392
COMMENT    Contact: Simon Hubbard
           Department of Biomolecular Sciences
           University of Manchester Institute of Science and Technology
           (UMIST)
           PO Box 88, Manchester, M60 1QD, UK
           Tel: 01612008930
           Fax: 01612360409
           Email: Simon.Hubbard@umist.ac.uk.

FEATURES
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constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Ronaldo et al., Genome Research 6
(1996) 791, except that a significantly longer
reannealing hybridization was used."

Query Match      16.8%; Score 87.8; DB 13; Length 801;
Best Local Similarity 88.8%; Pred. No. 3.9e-16;
Matches 95; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy      150  CGGTATCTGAGGGGACTAGGCTGTGTTTAGCGGAAAACGGGGCTTCGGTGTACGCGGT 209
Db      107  GCTTGACTGAGGCGACCATAGTATGATAGCGGAAGGCGGGCTTCGGTGTACGCGGT 48
Qy      210  TAGGAGTCCCTCAGCATATAGTATGCTTTCGTTTGCATAGGAGG 256

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Db      47  TAGGAGTCCCTCAGCATATAGTATGCTTTCGTTTGCATAGGAGTG 1
Qy      181  CGAAAACGGGGGCTTCGGTTCGTACGGGTAGGAGTCCCTCAGCATATAGTATGCTTCGC 240
Db      1  CGAAAACGGGGGCTTCGGTTCGTACGGGTAGGAGTCCCTCAGCATATAGTATGCTTCGC 60

Query Match      16.5%; Score 86.4; DB 13; Length 282;
Best Local Similarity 93.8%; Pred. No. 7e-16;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      241  TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAA 276
Db      61  TTTTGCATAGGAGGGGGAATGTAGTCAATAGAA 96

RESULT 35
BU471721/c
LOCUS   BU471721
DEFINITION BU471721 CSEQREN21 Gallus gallus CDNA clone CHEST257116 5', mRNA
sequence.
ACCESSION BU471721
VERSION   BU471721
KEYWORDS  EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Gallus gallus

REFERENCE
AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
           Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE     A Comprehensive Collection of Chicken cDNAs
JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE   22335534
PUBMED    12445392
COMMENT    Contact: Simon Hubbard
           Department of Biomolecular Sciences
           University of Manchester Institute of Science and Technology
           (UMIST)
           PO Box 88, Manchester, M60 1QD, UK
           Tel: 01612008930
           Fax: 01612360409
           Email: Simon.Hubbard@umist.ac.uk.

FEATURES
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   /mol_type="mRNA"
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   /tissue_type="Abdominal fat pad"
   /dev_stage="adult"
   /lab_host="DH10B"
   /clone_lib="CSEQRBL06"
   /note="Vector: pBluescript II KS(+); Site 1: EcoRI;
           Site 2: NotI; Modification of pBluescript II KS(+)
           [Stratagene] vector to accommodate cDNA produced with the
           T-trimmed protocol (Construction of uni-directionally
           cloned cDNA libraries from messenger RNA for improved 3'
           end DNA sequencing by Glenn Fu, et al. U.S. Patent #
           6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
           Ligate in double stranded adaptor containing BspI and
           BamHI sites [5'ggccgcgtcgagcccgatcgcaaaaaag]
           [5'aattctttttcgatccgggtgcagc]"

Query Match      16.5%; Score 86.4; DB 13; Length 282;
Best Local Similarity 93.8%; Pred. No. 7e-16;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      241  TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAA 276
Db      61  TTTTGCATAGGAGGGGGAATGTAGTCAATAGAA 96

RESULT 35
BU471721/c
LOCUS   BU471721
DEFINITION BU471721 CSEQREN21 Gallus gallus CDNA clone CHEST257116 5', mRNA
sequence.
ACCESSION BU471721
VERSION   BU471721
KEYWORDS  EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Gallus gallus

REFERENCE
AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
           Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE     A Comprehensive Collection of Chicken cDNAs
JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE   22335534
PUBMED    12445392
COMMENT    Contact: Simon Hubbard
           Department of Biomolecular Sciences
           University of Manchester Institute of Science and Technology
           (UMIST)
           PO Box 88, Manchester, M60 1QD, UK
           Tel: 01612008930
           Fax: 01612360409
           Email: Simon.Hubbard@umist.ac.uk.

FEATURES
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   /tissue_type="Abdominal fat pad"
   /dev_stage="adult"
   /lab_host="DH10B"
   /clone_lib="CSEQRBL06"
   /note="Vector: pBluescript II KS(+); Site 1: EcoRI;
           Site 2: NotI; Modification of pBluescript II KS(+)
           [Stratagene] vector to accommodate cDNA produced with the
           T-trimmed protocol (Construction of uni-directionally
           cloned cDNA libraries from messenger RNA for improved 3'
           end DNA sequencing by Glenn Fu, et al. U.S. Patent #
           6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
           Ligate in double stranded adaptor containing BspI and
           BamHI sites [5'ggccgcgtcgagcccgatcgcaaaaaag]
           [5'aattctttttcgatccgggtgcagc]"

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ACCESSION BU471721  
VERSION BU471721.1  
KEYWORDS GI:25965298  
SOURCE EST.  
ORGANISM Gallus gallus (chicken)

ORGANISM Gallus gallus (chicken)

## REFERENCE

1 (bases 1 to 766)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

## AUTHORS

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## MEDLINE

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(UMIST)

## PUBMED

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## COMMENT

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Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

## FEATURES

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## ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 766;  
Best Local Similarity 89.4%; Pred. No. 1e-15;  
Matches 93; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

## QY

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|||  
|||

## DB

108 GCTTACTGAGGCGGACCATAGTATGTATAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 49  
|||  
|||

## QY

210 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGGA 253  
|||  
|||

## DB

48 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGGA 5  
|||  
|||

## RESULT 36

BU243776  
LOCUS BU243776  
DEFINITION 603781634F1 CSEQCHN34 Gallus gallus cDNA clone CHEST731c9 5', mRNA  
sequence.

## ACCESSION

BU243776  
VERSION BU243776.1  
KEYWORDS GI:25491080  
SOURCE EST.  
ORGANISM Gallus gallus (chicken)

## ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 766;  
Best Local Similarity 89.4%; Pred. No. 1e-15;  
Matches 93; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

## QY

150 GCGTATCTGAGGCGACTAGGTCGTCTTAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 209  
|||  
|||

## DB

108 GCTTACTGAGGCGGACCATAGTATGTATAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 49  
|||  
|||

## QY

210 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGGA 253  
|||  
|||

## DB

48 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGGA 5  
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|||

## RESULT 37

BU349048  
LOCUS BU349048  
DEFINITION 604168720F1 CSEQCHN68 Gallus gallus cDNA clone CHEST10285 5', mRNA  
sequence.

## ACCESSION

BU349048  
VERSION BU349048.1  
KEYWORDS GI:25857049  
SOURCE EST.  
ORGANISM Gallus gallus (chicken)

## ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 780;  
Best Local Similarity 85.7%; Pred. No. 1.e-15;  
Matches 96; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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## DB

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## QY

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## DB

558 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGAGGGGAAA 609  
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## RESULT 37

BU349048  
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sequence.

## ACCESSION

BU349048  
VERSION BU349048.1  
KEYWORDS GI:25857049  
SOURCE EST.  
ORGANISM Gallus gallus (chicken)

## ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 780;  
Best Local Similarity 85.7%; Pred. No. 1.e-15;  
Matches 96; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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|||

## DB

498 GCTTACTGAGGCGGACCATAGTATGTATAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 557  
|||  
|||

## QY

210 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGAGGGGAAA 261  
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|||

## DB

558 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGAGGGGAAA 609  
|||  
|||

## REFERENCE

1 (bases 1 to 269)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

## AUTHORS

12445392  
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University of Manchester Institute of Science and Technology  
(UMIST)

## REFERENCE

1 (bases 1 to 780)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

## AUTHORS

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Contact: Simon Hubbard  
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## TITLE

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University of Manchester Institute of Science and Technology  
(UMIST)

## JOURNAL

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University of Manchester Institute of Science and Technology  
(UMIST)

## COMMENT

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Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

## FEATURES

1. .780  
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/dev stage="adult"  
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/note="Organ: liver; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## source

1. .780  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST731c9"  
/sex="Female"  
/dev stage="adult"  
/lab host="DH10B"  
/clone lib="CSEQCHN34"  
/note="Organ: liver; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 780;  
Best Local Similarity 85.7%; Pred. No. 1.e-15;  
Matches 96; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

## QY

150 GCGTATCTGAGGCGACTAGGTCGTCTTAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 209  
|||  
|||

## DB

498 GCTTACTGAGGCGGACCATAGTATGTATAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 557  
|||  
|||

## QY

210 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGAGGGGAAA 261  
|||  
|||

## DB

558 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGAGGGGAAA 609  
|||  
|||

## RESULT 37

BU349048  
LOCUS BU349048  
DEFINITION 604168720F1 CSEQCHN68 Gallus gallus cDNA clone CHEST10285 5', mRNA  
sequence.

## ACCESSION

BU349048  
VERSION BU349048.1  
KEYWORDS GI:25857049  
SOURCE EST.  
ORGANISM Gallus gallus (chicken)

## ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 780;  
Best Local Similarity 85.7%; Pred. No. 1.e-15;  
Matches 96; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

## QY

150 GCGTATCTGAGGCGACTAGGTCGTCTTAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 209  
|||  
|||

## DB

498 GCTTACTGAGGCGGACCATAGTATGTATAGCGGAAAGCGGGGCTTCGGTTGTCGCGGT 557  
|||  
|||

## QY

210 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGAGGGGAAA 261  
|||  
|||

## DB

558 TAGGAGTCCCTCAGCATATAGTATGCTTTGCTTTGTCATAGGAGGGGAAA 609  
|||  
|||

## REFERENCE

1 (bases 1 to 269)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

## AUTHORS

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(UMIST)

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Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@unist.ac.uk.

Location/Qualifiers

## FEATURES

source

1..516  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST992f15"  
/tissue\_type="whole embryo"  
/dev\_stage="20-21"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN03"  
/note="Organ: whole embryo; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 14.5%; Score 76; DB 13; Length 516;  
Best Local Similarity 89.4%; Pred. No. 1.6e-12;  
Matches 93; Conservative 0; Mismatches 10; Indels 1; Gaps 1;  
  
QY 150 GCGTATCTGAGGGAGTGGTGTAGGCGAAAGCGGGGCTTCGGTTGTACGCGGT 209  
Db 414 GTTCACTGAGGGAGCCATGATGATAGGCGAAGGC-GGGCTTCGGTTGTACGCGGT 472  
  
QY 210 TAGGAGTCCCTCAGCATATAGTATGCTTCGTTTGCATAGGGA 253  
Db 473 TAGGAGTCCCTCAGCATATAGTATGCTTCGTTTGCATAGGGA 516

RESULT 40  
BU491086 611 bp mRNA linear EST 30-NOV-2002  
LOCUS 604131646F1 CSQRB37 Gallus gallus cDNA clone CHEST959K12 5', mRNA  
DEFINITION sequence.  
ACCESSION BU491086  
VERSION BU491086.1 GI:25984663  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 611)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@unist.ac.uk.

## FEATURES

source

1..611

/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST959K12"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQR37"  
/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 14.3%; Score 74.8; DB 13; Length 611;  
Best Local Similarity 87.5%; Pred. No. 4.2e-12;  
Matches 105; Conservative 0; Mismatches 12; Indels 3; Gaps 2;  
  
QY 150 GCGTATCTGAGGGAGTGGTGTAGGCGAAAGCGGGGCTTCGGTTGTACGCGGT 209  
Db 485 GCTTCACTGAGGGAGCCATGATGATAGGCGAAGGC-GGGCTTCGGTTGTACGCGGT 543  
  
QY 210 TAGG-AGTCCCTCAGCATATAGTATGCTTCGTTTGCATAGGAGGGGAAATGAGT 267  
Db 544 TAGGAGTCCCTCAGCATATAGTATGCTTCGTTTGCATAGGAGGGGAAATGAGT 603

## RESULT 41

BU491487

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE

AUTHORS

1 (bases 1 to 647)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE 22335534

PUBMED 12445392

COMMENT

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Email: Simon.Hubbard@unist.ac.uk.

Location/Qualifiers

1..647

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST959K12"

/sex="Male and female"  
 /dev stage="adult"  
 /lab host="DH10B"  
 /clone lib="CSQREN37"  
 /note="Organ: pancreas; Vector: pBluescript II KS(+);  
 Site 1: EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand synthesis reaction,  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 14.1%; Score 73.8; DB 13; Length 647;  
 Best local similarity 84.1%; Pred. No. 8.9e-12;  
 Matches 95; Conservative 0; Mismatches 17; Indels 1; Gaps 1;  
 QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAAGCGGGCTTCGGTTTACGGGT 209  
 Db 485 GCTTGACGTAGGGGACCAAGTATGTATAGGCGAAAGCGGGCTTCGGTTTACGGGT 544  
 QY 210 TAGGAGTCCCTCCAGGATATAGTATTC-GCTTTTGATAGGCGGGGAA 261  
 Db 545 TAGGAGTCCCTCCAGGATATAGTATTCGGGCTTTTGATAGGCGGGGAA 597

## RESULT 42

LOCUS BU232252 774 bp mRNA linear EST 26-NOV-2002  
 DEFINITION 603410762F1 CSQCHN24 Gallus gallus cDNA clone CHEST327116 5', mRNA  
 sequence.  
 ACCESSION BU232252  
 VERSION BU232252.1 GI:25474766  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (Bases 1 to 774)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
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 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..774  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST327116"  
 /dev\_stage="22"  
 /lab\_host="DH10B"  
 /clone\_lib="CSQCHN24"  
 /note="Organ: head; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand synthesis reaction,  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 13.8%; Score 72.4; DB 13; Length 774;  
 Best local similarity 83.6%; Pred. No. 2.6e-11;  
 Matches 107; Conservative 0; Mismatches 16; Indels 5; Gaps 2;  
 QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAAGCGGGCTTCGGTTTACG 205  
 Db 513 GCTTGACGTAGGGGACCAAGTATGTATAGGCGAAAGCGGGCTTCGGTTTACG 672  
 QY 206 CGGTAGGAGTCCCTCCAGGATAT-AGTAGTTTCGCTTTTGATAGGCGGGGAAATGT 264  
 Db 673 CGGTAGGAGTCCCTCCAGGATATAGTAGTTTCGCTTTTGATAGGCGGGGAAATGT 732  
 QY 265 AGTCCTTAT 272  
 Db 733 AGTCCAAT 740

## RESULT 43

LOCUS BU416333 829 bp mRNA linear EST 29-NOV-2002  
 DEFINITION 603671314F1 CSEQRBL07 Gallus gallus cDNA clone CHEST616K3 5', mRNA  
 sequence.  
 ACCESSION BU416333  
 VERSION BU416333.1 GI:25909004  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (Bases 1 to 829)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..829  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST616K3"  
 /sex="Male and female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRBL07"  
 /note="Organ: pancreas; Vector: pBluescript II KS(+);  
 Site\_1: EcoRI; Site\_2: NotI; Modification of pBluescript  
 II KS(+) [Stratagene] vector to accommodate cDNA produced

with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites  
[5'aattcttttttcggatccggggtgcagc]

## ORIGIN

Query Match 13.6%; Score 71; DB 13; Length 829;  
Best Local Similarity 89.2%; Pred. No. 7.3e-11;  
Matches 99; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
  
QY 156 CTGAGGGAGCTAGGCTGTGTT-TAGGCGAAAGCGGG-CTTCGGTTGTACGGGTAGG 213  
DB CTGAGGGAGCTAGGCTGTGTT-TAGGCGAAAGCGGG-CTTCGGTTGTACGGGTAGG 767  
  
QY 214 ACTCCCTCAGCATATAGTTCGCTTTTGCATAGGAGGGGGAATGT 264  
DB AGTCCCTCAGCATATAGTTCGCTTTTGCATAGGAGGGGGAATGT 818

## RESULT 44

BU315394 773 bp mRNA linear EST 28-NOV-2002  
LOCUS 603853390F1 CSEQCHN62 Gallus gallus cDNA clone CHEST853C24 5', mRNA  
DEFINITION sequence.  
ACCESSION BU315394  
VERSION BU315394.1 GI:25823395  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

## REFERENCE

1 (bases 1 to 773)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

## PUBMED

12445392

## COMMENT

Contact: Simon Hubbard  
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PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

1..773  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, H1sex"  
/db\_xref="taxon:9031"  
/clone="CHEST853C24"  
/dev\_stage="36"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN62"

/note="Organ: heads; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 13.5%; Score 70.4; DB 13; Length 773;  
Best Local Similarity 83.3%; Pred. No. 1.1e-10;  
Matches 80; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
  
QY 161 GGGACCTAGGCTGTGTTTAGCGGAAAGCGGGCTTCGGTTGTACGGGTAGGATCCCC 220  
DB GGGACCTAGGCTGTGTTTAGCGGAAAGCGGGCTTCGGTTGTACGGGTAGGATCCCC 737  
  
QY 221 TCAGGATATAGTTCGCTTTTGCATAGGAGGG 256  
DB TCAGGATATAGTTCGCTTTTGCATAGGAGGG 773

## RESULT 45

BU490009 642 bp mRNA linear EST 30-NOV-2002  
LOCUS 604129112F1 CSEQCHN37 Gallus gallus cDNA clone CHEST953g3 5', mRNA  
DEFINITION sequence.  
ACCESSION BU490009  
VERSION BU490009.1 GI:25983586  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 642)

## REFERENCE

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

## PUBMED

12445392

## COMMENT

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

1..642  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST953g3"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN37"

/note="Organ: pancreas; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 13.4%; Score 70; DB 13; Length 642;

Best Local Similarity 89.3%; Pred. No. 1.4e-10;  
Matches 109; Conservative 0; Mismatches 10; Indels 3; Gaps 3;  
QY 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGCGGAAAAGCGGGCTTCGG-TTGTAGCGG 208  
|||  
Db 503 GCTTACTGAGGGGACCATAGTATGATAGGCGAAAAGCGGGCTTCGGTTGTAGCGCG 562  
|||  
QY 209 TTAGGAGT-CCCTCAGGATATAGTAGTTTGC-TTTTGCATAGGAGGGGAAAATGTAG 266  
|||  
Db 563 TTAGGAGTCCCTCAGGATATAGTAGTTTGCCTTTTGCATAGGAGGGGAAAATGTAG 622  
|||  
QY 267 TC 268  
|||  
Db 623 TC 624  
|||

RESULT 46  
LOCUS BU350008 848 bp mRNA linear EST 28-NOV-2002  
DEFINITION 603526141F1 CSEQCHN69 Gallus gallus cDNA clone CHEST473all 5', mRNA  
sequence.  
ACCESSION BU350008  
VERSION BU350008.1 GI:25858009  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 848)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A., and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
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University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..848  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST473all"  
/sex="Female"  
/tissue\_type="cerebellum"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN69"  
/note="Organ: brain; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 13.3%; Score 69.8; DB 13; Length 848;  
Best Local Similarity 89.3%; Pred. No. 1.4e-10;  
Matches 109; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

Best Local Similarity 87.6%; Pred. No. 1.8e-10;  
Matches 99; Conservative 0; Mismatches 12; Indels 2; Gaps 2;  
QY 161 GGGACTAGGCTGTGTTAGCGGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCC 220  
|||  
Db 625 GGGACATAGTATGATATAGGCGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGT-CCC 683  
|||  
QY 221 TCAGGATATAGTAGTTTGCCTTTTGCAT-AGGGAGGGGGAANTAGTCTTAT 272  
|||  
Db 684 TCAGGATATAGTAGTTTGCCTTTTGCATAGGAGGGGACATGTAGTCACAT 736  
|||

RESULT 47  
LOCUS BU403961 851 bp mRNA linear EST 27-NOV-2002  
DEFINITION 603482276F1 CSEQCHN59 Gallus gallus cDNA clone CHEST371520 5', mRNA  
sequence.  
ACCESSION BU403961  
VERSION BU403961.1 GI:25773017  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 851)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A., and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..851  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST371520"  
/dev\_stage="36"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN59"  
/note="Organ: limbs; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 13.2%; Score 69.2; DB 13; Length 851;  
Best Local Similarity 86.8%; Pred. No. 2.7e-10;  
Matches 99; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGCGGAAAAGCGGGCTTCGGTTGTAGCGGT 209  
|||  
Db 635 GCTTACTGAGGGGACCATAGTATGATATAGGCGGAGCGGGCTTCGGATGTAGCGGT 694  
|||

QY 210 TAGGAGTCCCTCAGGATA-TAGTAGTTTCGCTTTT-GCATAGGAGGGGAAA 261  
 Db |||||  
 695 TAGGAGTCCCTCAGGATA-TAGTAGTTTCGCTTTT-GCATAGGAGGGGAAA 748  
 |||||

RESULT 49  
 A1981988  
 LOCUS 647 bp mRNA linear EST 07-MAY-2001  
 DEFINITION pat.pk0070.g7.f chicken activated T cell cDNA Gallus gallus cdna  
 clone pat.pk0070.g7.f 5' similar to protein v-src, mRNA sequence.  
 ACCESSION A1981988  
 VERSION A1981988.1 GI:5885016  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE  
 A1981988  
 AUTHORS Tirunaguru,V.G., Sofer,L., Cui,J. and Burnside,J.  
 TITLE An expressed sequence tag database of T-cell-enriched activated chicken splenocytes: sequence analysis of 5251 clones  
 JOURNAL Genomics 66 (2), 144-151 (2000)  
 MEDLINE 20318616  
 PUBMED 10860659  
 COMMENT Contact: Joan Burnside  
 Molecular Endocrinology  
 University of Delaware  
 40 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302 831-1345  
 Fax: 302-831-3411  
 Email: joan@udel.edu, www.chickest.udel.edu  
 Seq primer: 47.

FEATURES  
 source  
 1..647  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="pat.pk0070.g7.f"  
 /sex="male"  
 /cell\_type="Con A-activated splenic T cell"  
 /lab\_host="E.coli TOP10 F"  
 /clone\_lib="chicken activated T cell cdna"  
 /note="vector: pcdNA3"

ORIGIN  
 Query Match 13.08; Score 68.2; DB 9; Length 647;  
 Best Local Similarity 69.28; Pred. No. 5e-10;  
 Matches 119; Conservative 0; Mismatches 51; Indels 2; Gaps 2;  
 QY 158 GAGGGGACTAGGGTGTGTTTGGCGAAAGCGGGGCTTCGGTTGTACCGGTTTAGGAGTC 217  
 Db |||||  
 407 GAGGGGACCATAGTATGTATAGCGAAAGCGGGGCTTCGGTTGTACCGGTTTAGGAGTC 466  
 QY 218 CCTCAGGATATAGTGTGTTTGGCGAAAGCGGGGCTTCGGTTGTACCGGTTTAGGAGTC 276  
 Db |||||  
 467 CCTCAGGATATAGTGTGTTTGGCGAAAGCGGGGCTTCGGTTGTACCGGTTTAGGAGTC 526  
 QY 277 TACTCTTGTAGTCTTTCACATGCTAGCATGATGATTTAGCATGCTTACA 328  
 Db |||||  
 527 GCCAGAGCA-ACCTGAAATATCTTAAAGACNATATAGGAAGAGGAGCA 577  
 |||||

RESULT 49  
 BU402803  
 LOCUS 630 bp mRNA linear EST 27-NOV-2002  
 DEFINITION 603485204F1 CSEQCHN59 Gallus gallus cdna clone CHEST378h1 5', mRNA  
 sequence.  
 ACCESSION BU402803  
 VERSION BU402803.1 GI:25771859  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 630)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 MEDLINE 12445392  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: simon.hubbard@umist.ac.uk.

FEATURES  
 source  
 1..630  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST378h1"  
 /dev\_stage="36"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN59"  
 /note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:  
 EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunt-ended, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Ronaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

ORIGIN  
 Query Match 12.78; Score 66.6; DB 13; Length 630;  
 Best Local Similarity 81.18; Pred. No. 1.6e-09;  
 Matches 90; Conservative 0; Mismatches 19; Indels 2; Gaps 1;  
 QY 150 GCCTATCTGAGGGGACTAGGGTGTGTTTGGCGAAAGCGGGGCTTCGGTTGTACCGGC- 208  
 Db |||||  
 462 GCTTGACTGAGGGGACCATAGTATGTATAGCGGAAGCGGGGCTTCGGTTGTACCGGC 521  
 QY 209 -TTAGAGTCCCTCAGGATATAGTATGCTTTTTCATAGGAGGGGG 258  
 Db |||||  
 522 TTCAGGAGTCCCTCAGGATATAGTATGCTTTTTCATAGGAGGGGG 572  
 |||||

RESULT 50  
 BU416401  
 LOCUS 619 bp mRNA linear EST 29-NOV-2002  
 DEFINITION 603551243F1 CSEQREL07 Gallus gallus cdna clone CHEST521e12 5', mRNA  
 sequence.  
 ACCESSION BU416401  
 VERSION BU416401.1 GI:25909072  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE  
 1 (bases 1 to 619)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,

(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).

Location/Qualifiers

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1. 376
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="ChEST206714"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="GSECOREN14"
```

Email: [stnoll.hubbard@umist.ac.uk](mailto:stnoll.hubbard@umist.ac.uk)

```

location/Qualifiers
1. .619
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST21e12"
/sex="Male and female"
/dev_stage="adult"
/lab_host="DH10B"

```

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/dev_stage="adult"  
/lab_host="DH10B"  
/clone_lib="CSEFORBN14"
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/note=Organ: ovary; Vector: pBluescript II KS(+); Site.1: EcoRI; Site.2: NotI; this normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntly ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 12.2%; Score 63.6; DB 13; Length 376;  
Best Local Similarity 93.6%; Pred. No. 1.1e-08;  
Matches 88; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

179	GGCCAAAGCGGGCTCGGTTCTTACGCGTTAGGAGTCCCTCAGGATATAGTAGTTTC	238
QY		
375	GCCAAAGCGGGCTCGGTTCTTACGCGTTAGGAGTCCCTCAGGATATAGTA-TTGC	318
DB		
239	GCTTTTGCATAGGAGGGGGAAATGTAGTCTTAT	272
QY		
317	GCTTTTGCATAGGAGGGGGAAATGTAGTCAAT	284
DB		

RESULT 52  
B0839774/C

LOCUS BQ839774 195 bp mRNA linear EST 09-AUG-2002  
DEFINITION H29 Chicken thyroid SSH library Gallus gallus clone H29  
similar to Avian leukosis virus strain ev-3, mRNA sequence.

ACCESSION BQ839774  
VERSION BQ839774.1 GI:22165701  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)

ORGANISM      Gallus gallus (chicken)

ORGANISM: *Gallus gallus*

Eukaryota; Metazoa; Chordata

Archosauria; Aves; Neogni

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 195)

**AUTHORS** Vasicek, D., Kaiser, P. and

# Analysis of expressed sequences

chickens affected with E

animal model of human Ha

JOURNAL  
Unpublished (2002)

COMMENT  
Contact: Kaiser P

Institute for Animal Health

Compton, Berkshire RG20

Tel: +44 1635 577263

Fax: +44 1635 577263

Email: [pete.kaiser@bbrc.org](mailto:pete.kaiser@bbrc.org)

Seq primer: T17

## SIGNATURES

source	1 195	1000000/2000000
1000000/2000000	1 195	1000000/2000000

7  
7  
4  
.  
.  
4

0  
0  
4  
5  
2  
0



/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Obese Strain (OS)"  
/db\_xref="taxon:9031"  
/clone="H29"  
/sex="male and female"  
/tissue\_type="thyroid"  
/clone\_lib="Chicken thyroid SSH library"  
/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH. Hybridisation was performed using the PCR-Select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

## ORIGIN

Query Match 12.1%; Score 63.2; DB 13; Length 195;  
Best Local Similarity 95.6%; Pred. No. 1.1e-08;  
Matches 65; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 205 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 264  
Db 195 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 136  
QY 265 AGTCTTAT 272  
Db 135 AGTCAAAAT 128

RESULT 53  
BQ839776/c  
LOCUS  
DEFINITION H30 chicken thyroid SSH library Gallus gallus cDNA clone H30  
similar to Avian leukosis virus strain ev-3, mRNA sequence.  
ACCESSION BQ839776.1 GI:22165703  
VERSION BQ839776.1  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE BQ839776 195 bp mRNA linear EST 09-AUG-2002  
AUTHORS Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
JOURNAL Phasianinae; Gallus.  
COMMENT Vasicek D., Kaiser P. and Hala, K.  
Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis  
Unpublished (2002)  
Contact: Kaiser P  
Institute for Animal Health  
Compton, Berkshire RG20 7NN, UK  
Tel: +44 1635 577263  
Fax: +44 1635 577263  
Email: pete.kaiser@bsrc.ac.uk  
Seq primer: T7.

FEATURES  
SOURCE

1..195  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Obese Strain (OS)"  
/db\_xref="taxon:9031"  
/clone="H30"  
/sex="male and female"  
/tissue\_type="thyroid"  
/clone\_lib="Chicken thyroid SSH library"  
/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system

## ORIGIN

Query Match 12.1%; Score 63.2; DB 13; Length 195;  
Best Local Similarity 95.6%; Pred. No. 1.1e-08;  
Matches 65; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 205 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 264  
Db 195 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 136  
QY 265 AGTCTTAT 272  
Db 135 AGTCAAAAT 128

RESULT 54  
BQ839779/c

LOCUS  
DEFINITION E31 Chicken thyroid SSH library Gallus gallus cDNA clone E31  
similar to Avian leukosis virus strain ev-3, mRNA sequence.  
ACCESSION BQ839779  
VERSION BQ839779.1 GI:22165706  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE BQ839779 195 bp mRNA linear EST 09-AUG-2002  
AUTHORS E31 Chicken thyroid SSH library Gallus gallus cDNA clone E31  
TITLE Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis  
Unpublished (2002)  
Contact: Kaiser P  
Institute for Animal Health  
Compton, Berkshire RG20 7NN, UK  
Tel: +44 1635 577263  
Fax: +44 1635 577263  
Email: pete.kaiser@bsrc.ac.uk  
Seq primer: T7.

FEATURES  
source

1..195  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Obese Strain (OS)"  
/db\_xref="taxon:9031"  
/clone="E31"  
/sex="male and female"  
/tissue\_type="thyroid"  
/clone\_lib="Chicken thyroid SSH library"  
/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH. Hybridisation was performed using the PCR-Select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

## ORIGIN

Query Match 12.1%; Score 63.2; DB 13; Length 195;  
Best Local Similarity 95.6%; Pred. No. 1.1e-08;  
Matches 65; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 205 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 264  
Db 195 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 136

(Qiagen), and used for SSH. Hybridisation was performed using the PCR-Select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

QY 265 AGTCTTAT 272  
 |||||  
 Db 135 AGTCAGAT 128

RESULT 55  
 BU414765  
 LOCUS 844 bp mRNA linear EST 29-NOV-2002  
 DEFINITION 603667837F1 CSEQRBL06 Gallus gallus cdna clone CHES760710 5', mRNA sequence.

ACCESSION BU414765  
 VERSION BU414765  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 844)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
 Location/Qualifiers  
 1..844  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHES760710"  
 /sex="Male and female"  
 /tissue\_type="Abdominal fat pad"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRBL06"  
 /notes="Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BglI and BamHI sites [5'ggcgcggtgcagcccggtatccgaaaaaag] [5'aattcttttttcgggtccgggtgcagc]"

ORIGIN  
 Query Match 12.0%; Score 62.8; DB 13; Length 844;  
 Best Local Similarity 79.1%; Pred. No. 2.8e-08;  
 Matches 87; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 150 GGTATCTAGAGGGAATAGGGTGTGTTAGGCGAAGCGGGCTTCGGTTACGGGT 209  
 |||||  
 Db 682 GCTTCACTAGAGGGAACCATAGTAATGTATAGGCGAAGCGGGCTCGTTTACGGGT 741  
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QY 210 TAGGAGTCCCTCAGGATATAGTAG-TTTCGCTTTTGCATAGGAGGGG 258  
 |||||  
 Db 742 TAGGAGTCCCTCAGGATATAGTAGTTGGCTTTTGCATAGGAGGGG 791  
 |||||

RESULT 56  
 BQ839752/c

LOCUS BQ839752 197 bp mRNA linear EST 09-AUG-2002  
 DEFINITION H24 Chicken thyroid SSH library Gallus gallus cdna clone H24 similar to Avian leukosis virus strain ev-3, mRNA sequence.

ACCESSION BQ839752  
 VERSION BQ839752.1 GI:22165679  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 197)  
 AUTHORS Vasicek, D., Kaiser, P. and Hala, K.  
 TITLE Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kaiser P  
 Institute for Animal Health  
 Compton, Berkshire RG20 7NN, UK  
 Tel: +44 1635 577263  
 Fax: +44 1635 577263  
 Email: pete.kaiser@ahrc.ac.uk  
 Seq primer: 17.

FEATURES  
 Location/Qualifiers  
 1..197  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:9031"  
 /clone="H24"  
 /sex="male and female"  
 /tissue\_type="thyroid"  
 /clone\_lib="Chicken thyroid SSH library"  
 /note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH hybridisation was performed using the PCR-Select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

ORIGIN  
 Query Match 11.9%; Score 62; DB 13; Length 197;  
 Best Local Similarity 92.9%; Pred. No. 2.7e-06;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 203 ACCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTGCATAGGAGGGGGAAT 262  
 |||||  
 Db 197 ACCGGTTAGGAGTCCCTCAGGATATAGTAGTGGCGCTTCGCTAGGAGGGGGAAT 138  
 |||||

QY 263 GTAGTCTTAT 272  
 |||||  
 Db 137 GTAGTCAAAAT 128  
 |||||

RESULT 57  
 BQ839750/c

LOCUS BQ839750 196 bp mRNA linear EST 09-AUG-2002  
 DEFINITION E24 Chicken thyroid SSH library Gallus gallus cdna clone E24 similar to Avian leukosis virus strain ev-3, mRNA sequence.

ACCESSION BQ839750  
 VERSION BQ839750.1 GI:22165677  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 196)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 TITLE Vasicek, D., Kaiser, P. and Hala, K.

**TITLE** Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis, an Unpublished (2002)

**JOURNAL COMMENT**  
Contact: Kaiser P  
Institute for Animal Health  
Compton, Berkshire RG20 7NN, UK  
Tel: +44 1635 577263  
Fax: +44 1635 577263  
Email: pete.kaiser@bbsrc.ac.uk  
Seq primer: T7.

# **FEATURES**

**source**  
1. .196  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Obese strain (OS)"  
/db\_xref="taxon:9031"  
/clone="E24"  
/sex="male and female"  
/tissue\_type="thyroid"  
/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH. Hybridisation was performed using the PCR-Select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

# **ORIGIN**

**Query Match** 11.5%; Score 60; DB 13; Length 196;  
**Best Local Similarity** 92.6%; Pred. No. 1.2e-07;  
**Matches** 63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 205 GCGGTAGAGTCCCTCAGGATATAGTAGTTTCGTTTCATGAGGAGGGAATCT 264  
196 GCGGTAGAGTCCCTCAGGATATAGTAGTTTCGTTTCATGAGGAGGGAATCT 137

**QY** 265 AGTCTTAT 272  
136 AGTCAAT 129

**RESULT 58**  
**BU314089**  
**LOCUS** 751 bp mRNA linear EST 28-NOV-2002  
**DEFINITION** BU314089.1 CSEQCHN61 Gallus gallus cDNA clone CHEST51906 5', mRNA sequence.

**ACCESSION** BU314089  
**VERSION** BU314089.1 GI:25822090  
**KEYWORDS** EST.  
**SOURCE** Gallus gallus (chicken)  
**ORGANISM** Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

**REFERENCE** 1 (bases 1 to 751)  
**AUTHORS** Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

**TITLE** A Comprehensive Collection of Chicken cDNAs  
**JOURNAL** Curr. Biol. 12 (22), 1965-1969 (2002)  
**MEDLINE** 22335534  
**PUBMED** 12445392

**COMMENT**  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

# **FEATURES**

## **source**

1. .751  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
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/sex="Female"  
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/lab\_host="DH10B"  
/clone\_lib="CSEQCHN61"

/note="Organ: heart; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

# **ORIGIN**

**Query Match** 10.8%; Score 56.6; DB 13; Length 751;  
**Best Local Similarity** 87.3%; Pred. No. 2.3e-06;  
**Matches** 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

**QY** 150 GCGTATCTGAGGGGACTAGGTGTGTTAGCGGAAAGCGGGCTTCGGTGTACGGGT 209  
680 GCTTGACTGAGGGACCATAGTAGTATAGCGGAGGCGGCTTCGGTGTACGGGT 739

**QY** 210 TAGGAGTCCCC 220  
**Db** 740 TAGGAGTCCCC 750

**RESULT 59**  
**BU124247**  
**LOCUS** 945 bp mRNA linear EST 25-NOV-2002  
**DEFINITION** BU124247.1 CSEQCHL18 Gallus gallus cDNA clone CHEST151124 5', mRNA sequence.

**ACCESSION** BU124247  
**VERSION** BU124247.1 GI:25334922  
**KEYWORDS** EST.  
**SOURCE** Gallus gallus (chicken)  
**ORGANISM** Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

**REFERENCE** 1 (bases 1 to 945)  
**AUTHORS** Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

**TITLE** A Comprehensive Collection of Chicken cDNAs  
**JOURNAL** Curr. Biol. 12 (22), 1965-1969 (2002)  
**MEDLINE** 22335534  
**PUBMED** 12445392

**COMMENT**  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

# **FEATURES**

## **source**

1. .945  
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/mol\_type="mRNA"  
/strain="Compton Line 151"



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Query Match      10.4%; Score 54.6; DB 13; Length 750;
Best Local Similarity 87.0%; Pred. No. 9.8e-06;
Matches 60; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 682 GCATTGACTGAGGGACCATAGTATGTATAGCGGAAGCGGGGCTTCGGTTGTACGGGT 741

742 TAGGAGTCC 750

RESULT 63				
BU413106				
LOCUS	BU413106	747 bp	mRNA	linear
				EST 29-NOV-2002

ACCESSION BU413106  
VERSION BU413106.1 GI:25905777  
KEYWORDS EST.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

MEDLINE 2235534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard

Tel: 01612008930  
 Fax: 01612360409  
 Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).

```

/db_xref="taxon:9031"
/clone="ChEST166b3"
/sex="Female"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQL05"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site:1: EcoRI; site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-timed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'-ggcgccgcgcacccggaaccgcaaaaaag] [5'aattcttttcttgcatcgtgcagc]
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	ORIGIN	
	Query Match	10.2%; Score 53.2; DB 13; Length 747;
	Best Local Similarity	94.6%; Pred. No. 2.7e-05;
	Matches 55; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	215 GTCCCTCAGGATATAGTAGTTTCGTCTTTCATAGGGGGGAATTAGTGCTTAT	272

ACCESSION	CF252511	CF252511.1	GI:33485766
VERSION	EST		
KEYWORDS			
SOURCE	Gallus gallus (chicken)		
ORGANISM	Gallus gallus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
AUTHORS	Witzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J., Chausse, A.M. and Zoorob, R.		
TITLE	A collection of chicken ESTs from activated immune cells		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Zoorob R UPR 1993 CNRS		
FEATURES	7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France Tel: 33 1 49 58 35 00 Fax: 33 1 49 58 33 81 Email: zoorob@vif.cnrs.fr		
source	Location/Qualifiers 1..725		
ORIGIN	/organism="Gallus gallus" /mol_type="mRNA" /db_xref="taxon:9031" /cell_line="HD11" /clone_lib="LPS-activated macrophage cell line" /note="Vector: pTriplex2"		
Query Match	9.0%; Score 47.2; DB 14; Length 725;		
Best Local Similarity	84.0%; Pred. No. 0.002;		
Matches	99; Conservative 0; Mismatches 13; Indels 4; Gaps 3;		
QY	148 TCCTATCTCAGGGGACTAGGGTGTGTTTAGGCGAAAGC-GGGGCTTCGGTTGTAGCG 206		
Db	584 TGGCTTAACTAAGGGGACTATGGCATGTATAGGCGTAAAGCGGGGCTTCGGTTGTAGCG 643		
QY	207 --GTTTAGGAGTCCCTC-AGCATAGTAGTTCGCTTTGCATA 249		
Db	644 CGGGTTAGGAGTCCCTCCTTAAGGATATAGTAGGCACGCTTTGCATA 689		
RESULT 66			
BU490848			
LOCUS	604130845F1 CSQRBN37 Gallus gallus cdna clone CHEST957112 5', mRNA	718 bp	linear EST 30-NOV-2002
DEFINITION	sequence.		
BU490848			
ACCESSION	BU490848.1	GI:25984425	
VERSION			
KEYWORDS	Gallus gallus (chicken)		
SOURCE	Gallus gallus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
REFERENCE	1 (bases 1 to 718)		
AUTHORS	Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.		
TITLE	A Comprehensive Collection of Chicken cDNAs		
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)		
MEDLINE	22335534		
PUBMED	12445392		
COMMENT	Contact: Simon Hubbard Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST) PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@umist.ac.uk		
FEATURES	Location/Qualifiers 1..719		
source			

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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST957112"
/sex="Male and female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRN37"
/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
ORIGIN
Query Match      8.9%; Score 46.8; DB 13; Length 718;
Best Local Similarity 88.6%; Pred. No. 0.0027;
Matches 62; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 156 CTGAGGGGACTAGGTGTGTAGCGGAAAGCGGGCTTCGGTTGTACGGGTAGGAG 215
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Db 650 CTGAGGGGACCATATGTATAGCGGAAAGCGGGCTTCGGTTGTACGGGTAGGAG 708

QY 216 TCCCTCAGG 225
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Db 709 TCCCTCAGG 718

RESULT 67
BU414295
LOCUS      724 bp mRNA linear EST 29-NOV-2002
DEFINITION 60368824F1 CSEQRN06 Gallus gallus cDNA clone CHEST609p5 5', mRNA sequence.
ACCESSION  BU414295
VERSION    BU414295.1 GI:2590693
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE  1 (bases 1 to 724)
AUTHORS   Boardman,P.E., Sanz-Exquerro,J., Overton,I.M., Burt,D.W., Bosch,B.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE     A Comprehensive Collection of Chicken cDNAs
JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE   22335534
PUBMED    12445392
COMMENT    Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
            Location/Qualifiers
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               /organism="Gallus gallus"
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               /strain="Layer and broiler"
               /db_xref="taxon:9031"
               /clone="CHEST609p5"

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/sex="Male and female"
/tissue_type="Abdominal fat pad"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRN06"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggcggtgcacccgcatccgaaaaaag] [5'aattcttttttcggatccgggggtgcacgc]"
ORIGIN
Query Match      8.9%; Score 46.6; DB 13; Length 724;
Best Local Similarity 79.5%; Pred. No. 0.0031;
Matches 93; Conservative 0; Mismatches 19; Indels 5; Gaps 3;

QY 150 CGGTATCTAGGGGACTAGGTGTGTAGCGGAAAGCGGGCTTCGGTTGTACCGGG 208
      |||||
Db 537 GCTTACTAGCGGGACCATATGTATAGCGGAAAGCGGGCTTCGGTTGTACCGGG 596

QY 209 TTAGGAGTCCCTC--AGGATATAGTATTTCGC--TTTTCATAGGAGGGGAAAA 261
      |||||
Db 597 TTAGGAAGTCCCTCAGGATATAGTATTTCGCCTTTTTCCTAGGAGGGGGGAA 653

RESULT 68
AB083460
LOCUS      401 bp mRNA linear EST 12-APR-2002
DEFINITION AB083460 Rattus norvegicus lactating adult Rattus norvegicus cDNA clone VP60 3', similar to Myeloblastosis-associated virus type 2 env gene (accession number: U10924.1), mRNA sequence.
ACCESSION  AB083460
VERSION    AB083460.1 GI:20144093
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 401)
AUTHORS   Yamashita,M., Glasgow,E., Zhang,B., Kusano,K. and Gainer,H.
TITLE     Identification of cell-specific mRNAs in oxytocinergic and vasopressinergic magnocellular neurons in rat supraoptic nucleus by single-cell differential hybridization
JOURNAL   Unpublished (2002)
COMMENT    Contact: Mitsuo Yamashita
            Department of Biotechnology
            Graduate School of Engineering, Osaka University
            2-1 Yamadaoka, Suita, Osaka 565-0871, Japan
            Tel: 81-6-6879-4170
            Fax: 81-6-6879-7418
            Email: yamashita@bio.eng.osaka-u.ac.jp.
            Location/Qualifiers
              1..401
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Query Match      8.7%; Score 45.4; DB 9; Length 401;
Best Local Similarity 55.3%; Pred. No. 0.0059;
Matches 109; Conservative 0; Mismatches 86; Indels 2; Gaps 1;

QY 185 AAGCGGGGCTTCGGTTGTACCGGG--TTAGGAGTCCCTCAGGATATAGTATTTCGCTT 242

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1	AAGCGGGCTCTCGTTGTAA	CGCGCTTAGGAAATCCCTCGAGGTATGCCAGATATGCTT	60
243	TTGCATAGGAGGGGGAAATAGTCTTATGCAATACCTTTGTGTCGTTCGCAATGGTA	302	
61	TTGCATAGGAGGGGGAAATGTGTCATATCATAGGTTAACTTTATATATACCAATAA	120	
303	ACGATGAGTTAGCAATGCGCTTACAAGAGAGAGAAAAGCACCGTCGTCGCGGATTTGGTG	362	
121	GGGAATCGCCTGATGATCGCCTGATGCCAAATAAGGTATTATATGATCCCATTTGGTG	180	
363	GAAGTAGGTGGTACGA	379	
181	GGCAAGGAGTGGCTGA	197	

RESULT	69
BU466407	
LOCUS	
DEFINITION	
ACCESSION	BU466407
VERSION	603373513F1 CSEQRBN20
KEYWORDS	Gallus gallus cdna clone CHEST28413 5', mRNA sequence.
SOURCE	EST.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 575)
REFERENCE	Boardman,P.B., Sanz-Exquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J. A Comprehensive Collection of Chicken cDNAs <i>Curr. Biol.</i> 12 (22), 1965-1969 (2002) 22335534 12445392
JOURNAL	Contact: Simon Hubbard
NEDLINE	Department of Biomolecular Sciences
PUBMED	University of Manchester Institute of Science and Technology (UMIST)
COMMENT	

## ORIGIN

Query Match	8.3%	Score 43.4	DB 13	Length 575
Best Local Similarity	82.0%	Prod. No. 0.029		
Matches	50	Conservative	0	Mismatches 11
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94	AATCTGCTTAGGTTAGGCGTTTTCGCTGCTTCGCGATGACGGCGACAGATATTCGCGT	153
QY		
224	AATATATTTAGGATTAGGCGTTTTCGCTGCTTCGCGATGACGGGTTAGGTGTGTGTGT	283
DB		
QY	154 A 154	
DB	284 A 284	

  

RESULT 70				
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LOCUS				
DEFINITION	pglin.px008.m21 Normalized Liver Library Gallus gallus cDNA clone			
	pglin.px008.m21 5' similar to pir J50432 J50432 transmembrane			
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	protein [Gallus gallus][G. mRNA sequence.			

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/ Note== vector: pcavsfok1 8
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Best Local Similarity 82.0%; Pred. No. 0.029;
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY      94  AATCTGCTTAGGGTTTAGCGCTTTTTCGGCTGCTTGCAGATGTACGGGCCAGATATTCGCGT 153
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Db      337  AATATATTAGGATTAGGCGGTTTTCGGCTGCTTCGCGATGTACGGGTTAGGTGTGTGTGTGT 396

QY      154  A 154
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Db      397  A 397

RESULT 71
BU258368
LOCUS
DEFINITION
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603743103F1 CQECHN38 Gallus gallus cDNA clone CHEST643f1 5', mRNA
sequence.
ACCESSION
BU258368
VERSION
BU258368.1 GI:25521250
KEYWORDS
EST.

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**AUTHORS** Jorge, E.C., Monteiro-Vitorello, C.B., Silva, C.S., Alves, H.J.,  
Patrião, M. and Coutinho, L.I.

**TITLE** Discovery of new genes in chicken embryos

**JOURNAL** Unpublished (2003)

**COMMENT** Contact: Erika C. Jorge  
Laboratory of Animal Biotechnology, Dep. of Animal Production  
EALQ - University of Sao Paulo  
Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
Tel: 55 19 3429 4434  
Fax: 55 19 3429 4285  
Email: ecjorge@ealq.usp.br  
PCR Primers  
REMARKS: T7.

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FEATURES
source
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cDNA library was constructed with the SuperScript Plasmid
System with Gateway Technology kit (Invitrogen), following
manufacturer's protocols. Plasmid DNA was purified using a
modified alkaline lysis method. Sequencing reactions were
conducted using the DYNAmic ET Dye Terminator sequencing
kit (Amersham Biosciences) according to the manufacturer's
recommendations. Clones were sequenced by the 5' end with
T7 primer. Sequencing reactions were analyzed on MegABACE
1000 automated DNA sequencer (Amersham Biosciences). The
quality and clustering of the ESTs were analyzed using the
software Phred/Gap3/Consed. Only EST sequences with Phred
quality greater than 20 and at least 200 bp were
considered for clustering."

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QY	94	AATCTGTTAGCGTTTACGGCTTCCTTGCGGTGCTGCAGTACGGCCCAKATATCCT	
Db	473	AATATATTAGCATTTAGCGCTTTTCGCTGCTTCGCGATGTACGGGTAGGTGTGTGTGT	532
QY	154	A 154	
Db	533	A 533	

VERSION	BU412768.1	GI:25905439
KEYWORDS	EST.	
SOURCE	Gallus gallus (chicken)	
ORGANISM	Gallus gallus	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	
	Phasianinae; Gallus.	
REFERENCE	1 (bases 1 to 662)	
AUTHORS	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.	
TITLE	A Comprehensive Collection of Chicken cDNAs	
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)	
MEDLINE	22395534	
PUBMED	12445392	

COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES source  
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/note="Organ: ovary; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
[Stratagene] vector to accommodate cDNA produced with the  
T-trimmed protocol (Construction of uni-directionally  
cloned cDNA libraries from messenger RNA for improved 3'  
end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
Ligate in double stranded adaptor containing BspI and  
BamHI sites [5'ggcgcgtgcagccgcgacccgaaaaag]  
[5'aattcttttttcggatcgagggtgcagc]"

ORIGIN  
Query Match 8.3%; Score 43.4; DB 13; Length 662;  
Best Local Similarity 82.0%; Pred. No. 0.03;  
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 94 AATCTGCTTAGGTTAGCGTTTGGCTGCTTCGCGATGTCAGCGCCAGATATTCGCGT 153  
Db 306 AATATATTAGGATTAGCGTTTGGCTGCTTCGCGATGTCAGCGTTAGGTGTGTGT 365  
QY 154 A 154  
Db 366 A 366  
RESULT 74  
BU238874 684 bp mRNA linear EST 26-NOV-2002  
LOCUS 603322034F1 CSEQCHN33 Gallus gallus cDNA clone CHEST249c9 5', mRNA  
DEFINITION sequence.  
ACCESSION BU238874.1 GI:25484934  
VERSION BU238874.1  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 684)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL A Comprehensive Collection of Chicken cDNAs  
MEDLINE Curr. Biol. 12 (22), 1965-1969 (2002)  
PUBMED 22335534  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES source  
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EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN  
Query Match 8.3%; Score 43.4; DB 13; Length 684;  
Best Local Similarity 82.0%; Pred. No. 0.031;  
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 94 AATCTGCTTAGGTTAGCGTTTGGCTGCTTCGCGATGTCAGCGCCAGATATTCGCGT 153  
Db 361 AATATATTAGGATTAGCGTTTGGCTGCTTCGCGATGTCAGCGTTAGGTGTGTGT 420  
QY 154 A 154  
Db 421 A 421  
RESULT 75  
BU476993 704 bp mRNA linear EST 30-NOV-2002  
LOCUS 603845910F1 CSEQREN22 Gallus gallus cDNA clone CHEST834d3 5', mRNA  
DEFINITION sequence.  
ACCESSION BU476993  
VERSION BU476993.1 GI:25970570  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 704)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL A Comprehensive Collection of Chicken cDNAs  
MEDLINE Curr. Biol. 12 (22), 1965-1969 (2002)  
PUBMED 22335534  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES source  
1. .704  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="layer and broiler"  
/db\_xref="taxon:9031"

Fri Mar 12 09:26:03 2004

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/clone="CHEST834d3"
/sex="Male and female"
/tissue type="Chondrocytes isolated from growth plate
cartilage"
/dev stage="adult"
/lab host="DH10B"
/clone lib="CSEQRAN22"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

```

# ORIGIN

Query Match 8.3%; Score 43.4; DB 13; Length 704;  
 Best Local Similarity 82.0%; Pred. No. 0.031;  
 Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 94 AATCTGCTTAGGGTTAGCGCTTTTGGCTGCTTCGGATGATCGGGCCAGATATTCGCGT 153
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Db 467 AATATATTTAGGATTAGCGCTTTTGGCTGCTTCGGATGATCGGGTTAGGTGTGTGT 526

QY 154 A 154
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Db 527 A 527

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Search completed: March 11, 2004, 11:07:05  
 Job time : 3128.7 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:54:28 ; Search time 1476.54 Seconds  
(without alignments)  
7749.596 Million cell updates/sec

Title: US-09-733-368a-1\_COPY\_349\_612  
Perfect score: 264  
Sequence: 1 atgtagcttcattgcaatac.....accacatgggtgcacctc 264

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

GenEmbl:

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pin.\*
- 35: em.htg.rod.\*
- 36: em.htg.man.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	100.0	648	6	AX175190 Sequence
2	264	100.0	648	6	AX175195 Sequence
c	262.4	99.4	7086	6	AX743955 Sequence
3	262.4	99.4	8238	6	BD268239 Adenoviru
4	262.4	99.0	330	14	ALRSV40LTR
5	261.4	99.0	700	14	ALRDCV
6	261.4	99.0	700	14	REASV3
7	261.4	99.0	1239	14	ALRDA1
8	261.4	99.0	3256	14	ALRDA2
9	261.4	99.0	11572	12	ABI05370
10	261.4	99.0	11627	6	BD261584
11	260.4	98.6	2245	6	AX643582
12	260.4	98.6	6289	12	XXU42373
13	259.2	98.2	5177	6	AX018983
14	259.2	98.2	5177	6	BD136828
15	259.2	97.8	1016	14	REASV3
16	257.6	97.6	4965	6	AR071323
17	257.2	97.4	262	6	AX256413
18	256.4	97.1	562	6	AX643583
19	256.4	95.2	4457	6	AX743954
20	251.4	95.2	7334	6	AX743956
c	251.4	95.2	7334	6	AX743956
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22	248.2	94.0	4341	6	AX286570
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24	248.2	94.0	4341	6	AX286570
25	248.2	94.0	4341	6	AX286570
26	248.2	94.0	4341	6	AX286570
27	248.2	94.0	4341	6	AX286570
28	248.2	94.0	4341	6	AX286570
29	248.2	94.0	4341	6	AX286570
30	248.2	94.0	4341	6	AX286570
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32	248.2	94.0	4341	6	AX286570
c	248.2	94.0	4341	6	AX286570
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34	248.2	94.0	4341	6	AX286570
35	248.2	94.0	4341	6	AX286570
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43	248.2	94.0	4341	6	AX286570
44	248.2	94.0	4341	6	AX286570
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46	248.2	94.0	4341	6	AX286570
47	248.2	94.0	4341	6	AX286570
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